

SEQUENCE LISTING

<110> Chang, Chawnshang

<120> Androgen Receptor Coregulators

<130> 21108.0011U6

<140> 10/517,155

<141> 2005-01-06

<150> PCT/US03/17937

<151> 2003-06-06

<150> US 60/387,087

<151> 2002-06-06

<160> 47

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1721

<212> DNA

<213> Homo sapien

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<221> CDS

<222> (40)...(1464)

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<222> (1120)...(1452)

<223> Coding sequence and polypeptide region for the  
C-terminal domain

<220>

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<222> (697)...(834)

<223> Coding sequence and polypeptide region which may  
form a cystein-rich RING finger motif

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<222> (964)...(1089)

<223> Coding sequence and polypeptide region for a  
cystein-rich B box like structure

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				1			5		

cga	gaa	gct	cag	gag	gat	gaa	ttg	ctg	gcc	ctg	gca	agt	att	tac	gat	102
Arg	Glu	Ala	Gln	Glu	Asp	Glu	Leu	Leu	Ala	Leu	Ala	Ser	Ile	Tyr	Asp	
			10					15						20		

gga gat gaa ttt aga aaa gca gag tct gtc caa ggt gga gaa acc agg Gly Asp Glu Phe Arg Lys Ala Glu Ser Val Gln Gly Gly Glu Thr Arg 25 30 35	150
atc tat ttg gat ttg cca cag aat ttc aag ata ttt gtg agc ggc aat Ile Tyr Leu Asp Leu Pro Gln Asn Phe Lys Ile Phe Val Ser Gly Asn 40 45 50	198
tca aat gag tgt ctc cag aat agt ggc ttt gaa tac acc att tgc ttt Ser Asn Glu Cys Leu Gln Asn Ser Gly Phe Glu Tyr Thr Ile Cys Phe 55 60 65	246
ctg cct cca ctt gtg ctg aac ttt gaa ctg cca cca gat tat cca tcc Leu Pro Pro Leu Val Leu Asn Phe Glu Leu Pro Pro Asp Tyr Pro Ser 70 75 80 85	294
tct tcc cca cct tca ttc aca ctt agt ggc aaa tgg ctg tca cca act Ser Ser Pro Pro Ser Phe Thr Leu Ser Gly Lys Trp Leu Ser Pro Thr 90 95 100	342
cag cta tct gct cta tgc aag cac tta gac aac cta tgg gaa gaa cac Gln Leu Ser Ala Leu Cys Lys His Leu Asp Asn Leu Trp Glu Glu His 105 110 115	390
cgt ggc agc gtg gtc ctg ttt gcc tgg atg caa ttt ctt aag gaa gag Arg Gly Ser Val Val Leu Phe Ala Trp Met Gln Phe Leu Lys Glu Glu 120 125 130	438
acc cta gca tac ttg aat att gtc tct cct ttt gag ctc aag att ggt Thr Leu Ala Tyr Leu Asn Ile Val Ser Pro Phe Glu Leu Lys Ile Gly 135 140 145	486
tct cag aaa aaa gtg cag aga agg aca gct caa gct tct ccc aac aca Ser Gln Lys Lys Val Gln Arg Arg Thr Ala Gln Ala Ser Pro Asn Thr 150 155 160 165	534
gag cta gat ttt gga gga gct gct gga tct gat gta gac caa gag gaa Glu Leu Asp Phe Gly Gly Ala Ala Gly Ser Asp Val Asp Gln Glu Glu 170 175 180	582
att gtg gat gag aga gca gtg cag gat gtg gaa tca ctg tca aat ctg Ile Val Asp Glu Arg Ala Val Gln Asp Val Glu Ser Leu Ser Asn Leu 185 190 195	630
atc cag gaa atc ttg gac ttt gat caa gct cag cag ata aaa tgc ttt Ile Gln Glu Ile Leu Asp Phe Asp Gln Ala Gln Gln Ile Lys Cys Phe 200 205 210	678
aat agt aaa ttg ttc ctg tgc agt atc tgt ttc tgt gag aag ctg ggt Asn Ser Lys Leu Phe Leu Cys Ser Ile Cys Phe Cys Glu Lys Leu Gly 215 220 225	726
agt gaa tgc atg tac ttc ttg gag tgc agg cat gtg tac tgc aaa gcc Ser Glu Cys Met Tyr Phe Leu Glu Cys Arg His Val Tyr Cys Lys Ala 230 235 240 245	774
tgt ctg aag gac tac ttt gaa atc cag atc aga gat ggc cag gtt caa Cys Leu Lys Asp Tyr Phe Glu Ile Gln Ile Arg Asp Gly Gln Val Gln 250 255 260	822

tgc ctc aac tgc cca gaa cca aag tgc cct tcg gtg gcc act cct ggt Cys Leu Asn Cys Pro Glu Pro Lys Cys Pro Ser Val Ala Thr Pro Gly 265 270 275	870
cag gtc aaa gag tta gtg gaa gca gag tta ttt gcc cgt tat gac cgc Gln Val Lys Glu Leu Val Glu Ala Glu Leu Phe Ala Arg Tyr Asp Arg 280 285 290	918
ctt ctc ctc cag tcc tcc ttg gac ctg atg gca gat gtg gtg tac tgc Leu Leu Leu Gln Ser Ser Leu Asp Leu Met Ala Asp Val Val Tyr Cys 295 300 305	966
ccc cgg ccg tgc tgc cag ctg cct gtg atg cag gaa cct ggc tgc acc Pro Arg Pro Cys Cys Gln Leu Pro Val Met Gln Glu Pro Gly Cys Thr 310 315 320 325	1014
atg ggt atc tgc tcc agc tgc aat ttt gcc ttc tgt act ttg tgc agg Met Gly Ile Cys Ser Ser Cys Asn Phe Ala Phe Cys Thr Leu Cys Arg 330 335 340	1062
ttg acc tac cat ggg gtc tcc cca tgt aag gtg act gca gag aaa tta Leu Thr Tyr His Gly Val Ser Pro Cys Lys Val Thr Ala Glu Lys Leu 345 350 355	1110
atg gac tta cga aat gaa tac ctg caa gcg gat gag gct aat aaa aga Met Asp Leu Arg Asn Glu Tyr Leu Gln Ala Asp Glu Ala Asn Lys Arg 360 365 370	1158
ctt ttg gat caa agg tat ggt aag aga gtg att cag aag gca ctg gaa Leu Leu Asp Gln Arg Tyr Gly Lys Arg Val Ile Gln Lys Ala Leu Glu 375 380 385	1206
gag atg gaa agt aag gag tgg cta gag aag aac tca aag agc tgc cca Glu Met Glu Ser Lys Glu Trp Leu Glu Lys Asn Ser Lys Ser Cys Pro 390 395 400 405	1254
tgt tgt gga act ccc ata gag aaa tta gac gga tgt aac aag atg aca Cys Cys Gly Thr Pro Ile Glu Lys Leu Asp Gly Cys Asn Lys Met Thr 410 415 420	1302
tgt act ggc tgt atg caa tat ttc tgt tgg att tgc atg ggt tct ctc Cys Thr Gly Cys Met Gln Tyr Phe Cys Trp Ile Cys Met Gly Ser Leu 425 430 435	1350
tct aga gca aac cct tac aaa cat ttc aat gac cct ggt tca cca tgt Ser Arg Ala Asn Pro Tyr Lys His Phe Asn Asp Pro Gly Ser Pro Cys 440 445 450	1398
ttt aac cgg ctg ttt tat gct gtg gat gtt gac gac gat att tgg gaa Phe Asn Arg Leu Phe Tyr Ala Val Asp Val Asp Asp Asp Ile Trp Glu 455 460 465	1446
gat gag gta gaa gac tag ttaactactg ctcaagatat ttaactactg Asp Glu Val Glu Asp *	1494
470	
ctcaagatat ggaagtggat tgtttttccc taatcttccg tcaagtacac aaagtaactt	1554
tgccgggatatt ttagggtact attcattcac tcttctgtcg tagaagatat ggaagaacga	1614
ggtttatatt ttcatgtggt actactgaag aagggtgcatt gatacatattt taaatgtaag	1674
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 <212> PRT  
 <213> Homo sapien

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 Gly Gly Glu Thr Arg Ile Tyr Leu Asp Leu Pro Gln Asn Phe Lys Ile  
 35 40 45  
 Phe Val Ser Gly Asn Ser Asn Glu Cys Leu Gln Asn Ser Gly Phe Glu  
 50 55 60  
 Tyr Thr Ile Cys Phe Leu Pro Pro Leu Val Leu Asn Phe Glu Leu Pro  
 65 70 75 80  
 Pro Asp Tyr Pro Ser Ser Ser Pro Pro Ser Phe Thr Leu Ser Gly Lys  
 85 90 95  
 Trp Leu Ser Pro Thr Gln Leu Ser Ala Leu Cys Lys His Leu Asp Asn  
 100 105 110  
 Leu Trp Glu Glu His Arg Gly Ser Val Val Leu Phe Ala Trp Met Gln  
 115 120 125  
 Phe Leu Lys Glu Glu Thr Leu Ala Tyr Leu Asn Ile Val Ser Pro Phe  
 130 135 140  
 Glu Leu Lys Ile Gly Ser Gln Lys Lys Val Gln Arg Arg Thr Ala Gln  
 145 150 155 160  
 Ala Ser Pro Asn Thr Glu Leu Asp Phe Gly Gly Ala Ala Gly Ser Asp  
 165 170 175  
 Val Asp Gln Glu Glu Ile Val Asp Glu Arg Ala Val Gln Asp Val Glu  
 180 185 190  
 Ser Leu Ser Asn Leu Ile Gln Glu Ile Leu Asp Phe Asp Gln Ala Gln  
 195 200 205  
 Gln Ile Lys Cys Phe Asn Ser Lys Leu Phe Leu Cys Ser Ile Cys Phe  
 210 215 220  
 Cys Glu Lys Leu Gly Ser Glu Cys Met Tyr Phe Leu Glu Cys Arg His  
 225 230 235 240  
 Val Tyr Cys Lys Ala Cys Leu Lys Asp Tyr Phe Glu Ile Gln Ile Arg  
 245 250 255  
 Asp Gly Gln Val Gln Cys Leu Asn Cys Pro Glu Pro Lys Cys Pro Ser  
 260 265 270  
 Val Ala Thr Pro Gly Gln Val Lys Glu Leu Val Glu Ala Glu Leu Phe  
 275 280 285  
 Ala Arg Tyr Asp Arg Leu Leu Leu Gln Ser Ser Leu Asp Leu Met Ala  
 290 295 300  
 Asp Val Val Tyr Cys Pro Arg Pro Cys Cys Gln Leu Pro Val Met Gln  
 305 310 315 320  
 Glu Pro Gly Cys Thr Met Gly Ile Cys Ser Ser Cys Asn Phe Ala Phe  
 325 330 335  
 Cys Thr Leu Cys Arg Leu Thr Tyr His Gly Val Ser Pro Cys Lys Val  
 340 345 350  
 Thr Ala Glu Lys Leu Met Asp Leu Arg Asn Glu Tyr Leu Gln Ala Asp  
 355 360 365  
 Glu Ala Asn Lys Arg Leu Leu Asp Gln Arg Tyr Gly Lys Arg Val Ile  
 370 375 380  
 Gln Lys Ala Leu Glu Glu Met Glu Ser Lys Glu Trp Leu Glu Lys Asn  
 385 390 395 400  
 Ser Lys Ser Cys Pro Cys Cys Gly Thr Pro Ile Glu Lys Leu Asp Gly  
 405 410 415  
 Cys Asn Lys Met Thr Cys Thr Gly Cys Met Gln Tyr Phe Cys Trp Ile  
 420 425 430

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Cys Met Gly Ser Leu Ser Arg Ala Asn Pro Tyr Lys His Phe Asn Asp
      435                440                445
Pro Gly Ser Pro Cys Phe Asn Arg Leu Phe Tyr Ala Val Asp Val Asp
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Asp Asp Ile Trp Glu Asp Glu Val Glu Asp
465                470

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<222> (1)...(1335)

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<222> (750)...(1332)
<223> Coding sequence and polypeptide region for the
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<222> (631)...(783)
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<222> (808)...(996)
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<220>
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Met Pro Arg Ser Gly Ala Pro Lys Glu Arg Pro Ala Glu Pro Leu Thr
  1                5                10                15

cct ccc cca tcc tat ggc cac cag cca aca ggg cag tct ggg gag tct      96
Pro Pro Pro Ser Tyr Gly His Gln Pro Thr Gly Gln Ser Gly Glu Ser
      20                25                30

tca gga gcc tcg ggg gac aag gac cac ctg tac agc acg gta tgc aag      144
Ser Gly Ala Ser Gly Asp Lys Asp His Leu Tyr Ser Thr Val Cys Lys
      35                40                45

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cct cgg tcc cca aag cct gca gcc ccg gcc gcc cct cca ttc tcc tct Pro Arg Ser Pro Lys Pro Ala Ala Pro Ala Ala Pro Pro Phe Ser Ser 50 55 60	192
tcc agc ggt gtc ttg ggt acc ggg ctc tgt gag cta gat cgg ttg ctt Ser Ser Gly Val Leu Gly Thr Gly Leu Cys Glu Leu Asp Arg Leu Leu 65 70 75 80	240
cag gaa ctt aat gcc act cag ttc aac atc aca gat gaa atc atg tct Gln Glu Leu Asn Ala Thr Gln Phe Asn Ile Thr Asp Glu Ile Met Ser 85 90 95	288
cag ttc cca tct agc aag gtg gct tca gga gag cag aag gag gac cag Gln Phe Pro Ser Ser Lys Val Ala Ser Gly Glu Gln Lys Glu Asp Gln 100 105 110	336
tct gaa gat aag aaa aga ccc agc ctc cct tcc agc ccg tct cct ggc Ser Glu Asp Lys Lys Arg Pro Ser Leu Pro Ser Ser Pro Ser Pro Gly 115 120 125	384
ctc cca aag gct tct gcc acc tca gcc act ctg gag ctg gat aga ctg Leu Pro Lys Ala Ser Ala Thr Ser Ala Thr Leu Glu Leu Asp Arg Leu 130 135 140	432
atg gcc tca ctc cct gac ttc cgc gtt caa aac cat ctt cca gcc tct Met Ala Ser Leu Pro Asp Phe Arg Val Gln Asn His Leu Pro Ala Ser 145 150 155 160	480
ggg cca act cag cca ccg gtg gtg agc tcc aca aat gag ggc tcc cca Gly Pro Thr Gln Pro Pro Val Val Ser Ser Thr Asn Glu Gly Ser Pro 165 170 175	528
tcc cca cca gag ccg act gca aag ggc agc cta gac acc atg ctg ggg Ser Pro Pro Glu Pro Thr Ala Lys Gly Ser Leu Asp Thr Met Leu Gly 180 185 190	576
ctg ctg cag tcc gac ctc agc cgc cgg ggt gtt ccc acc cag gcc aaa Leu Leu Gln Ser Asp Leu Ser Arg Arg Gly Val Pro Thr Gln Ala Lys 195 200 205	624
ggc ctc tgt ggc tcc tgc aat aaa cct att gct ggg caa gtg gtg acg Gly Leu Cys Gly Ser Cys Asn Lys Pro Ile Ala Gly Gln Val Val Thr 210 215 220	672
gct ctg ggc cgc gcc tgg cac ccc gag cac ttc gtt tgc gga ggc tgt Ala Leu Gly Arg Ala Trp His Pro Glu His Phe Val Cys Gly Gly Cys 225 230 235 240	720
tcc acc gcc ctg gga ggc agc agc ttc ttc gag aag gat gga gcc ccc Ser Thr Ala Leu Gly Gly Ser Ser Phe Phe Glu Lys Asp Gly Ala Pro 245 250 255	768
ttc tgc ccc gag tgc tac ttt gag cgc ttc tcg cca aga tgt ggc ttc Phe Cys Pro Glu Cys Tyr Phe Glu Arg Phe Ser Pro Arg Cys Gly Phe 260 265 270	816
tgc aac cag ccc atc cga cac aag atg gtg acc gcc ttg ggc act cac Cys Asn Gln Pro Ile Arg His Lys Met Val Thr Ala Leu Gly Thr His 275 280 285	864

tgg cac cca gag cat ttc tgc tgc gtc agt tgc ggg gag ccc ttc gga	912
Trp His Pro Glu His Phe Cys Cys Val Ser Cys Gly Glu Pro Phe Gly	
290 295 300	
gat gag ggt ttc cac gag cgc gag ggc cgc ccc tac tgc cgc cgg gac	960
Asp Glu Gly Phe His Glu Arg Glu Gly Arg Pro Tyr Cys Arg Arg Asp	
305 310 315 320	
ttc ctg cag ctg ttc gcc ccg cgc tgc cag ggc tgc cag ggc ccc atc	1008
Phe Leu Gln Leu Phe Ala Pro Arg Cys Gln Gly Cys Gln Gly Pro Ile	
325 330 335	
ctg gat aac tac atc tcg gcg ctc agc ctg ctc tgg cac ccg gac tgt	1056
Leu Asp Asn Tyr Ile Ser Ala Leu Ser Leu Leu Trp His Pro Asp Cys	
340 345 350	
ttc gtc tgc agg gaa tgc ttc gcg ccc ttc tcg gga ggc agc ttt ttc	1104
Phe Val Cys Arg Glu Cys Phe Ala Pro Phe Ser Gly Gly Ser Phe Phe	
355 360 365	
gag cac gag ggc cgc ccg ttg tgc gag aac cac ttc cac gca cga cgc	1152
Glu His Glu Gly Arg Pro Leu Cys Glu Asn His Phe His Ala Arg Arg	
370 375 380	
ggc tcg ctg tgc ccc acg tgt ggc ctc cct gtg acc ggc cgc tgc gtg	1200
Gly Ser Leu Cys Pro Thr Cys Gly Leu Pro Val Thr Gly Arg Cys Val	
385 390 395 400	
tcg gcc ctg ggt cgc cgc ttc cac ccg gac cac ttc gca tgc acc ttc	1248
Ser Ala Leu Gly Arg Arg Phe His Pro Asp His Phe Ala Cys Thr Phe	
405 410 415	
tgc ctg cgc ccg ctc acc aag ggg tcc ttc cag gag cgc gcc ggc aag	1296
Cys Leu Arg Pro Leu Thr Lys Gly Ser Phe Gln Glu Arg Ala Gly Lys	
420 425 430	
ccc tac tgc cag ccc tgc ttc ctg aag ctc ttc ggc tga	1335
Pro Tyr Cys Gln Pro Cys Phe Leu Lys Leu Phe Gly	
435 440	

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<212> PRT

<213> Homo sapien

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Met Pro Arg Ser Gly Ala Pro Lys Glu Arg Pro Ala Glu Pro Leu Thr	
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20 25 30	
Ser Gly Ala Ser Gly Asp Lys Asp His Leu Tyr Ser Thr Val Cys Lys	
35 40 45	
Pro Arg Ser Pro Lys Pro Ala Ala Pro Ala Ala Pro Pro Phe Ser Ser	
50 55 60	
Ser Ser Gly Val Leu Gly Thr Gly Leu Cys Glu Leu Asp Arg Leu Leu	
65 70 75 80	
Gln Glu Leu Asn Ala Thr Gln Phe Asn Ile Thr Asp Glu Ile Met Ser	
85 90 95	

Gln	Phe	Pro	Ser	Ser	Lys	Val	Ala	Ser	Gly	Glu	Gln	Lys	Glu	Asp	Gln	100	105	110
Ser	Glu	Asp	Lys	Lys	Arg	Pro	Ser	Leu	Pro	Ser	Ser	Pro	Ser	Pro	Gly	115	120	125
Leu	Pro	Lys	Ala	Ser	Ala	Thr	Ser	Ala	Thr	Leu	Glu	Leu	Asp	Arg	Leu	130	135	140
Met	Ala	Ser	Leu	Pro	Asp	Phe	Arg	Val	Gln	Asn	His	Leu	Pro	Ala	Ser	145	150	155
Gly	Pro	Thr	Gln	Pro	Pro	Val	Val	Ser	Ser	Thr	Asn	Glu	Gly	Ser	Pro	165	170	175
Ser	Pro	Pro	Glu	Pro	Thr	Ala	Lys	Gly	Ser	Leu	Asp	Thr	Met	Leu	Gly	180	185	190
Leu	Leu	Gln	Ser	Asp	Leu	Ser	Arg	Gly	Val	Pro	Thr	Gln	Ala	Lys		195	200	205
Gly	Leu	Cys	Gly	Ser	Cys	Asn	Lys	Pro	Ile	Ala	Gly	Gln	Val	Val	Thr	210	215	220
Ala	Leu	Gly	Arg	Ala	Trp	His	Pro	Glu	His	Phe	Val	Cys	Gly	Gly	Cys	225	230	235
Ser	Thr	Ala	Leu	Gly	Gly	Ser	Ser	Phe	Phe	Glu	Lys	Asp	Gly	Ala	Pro	245	250	255
Phe	Cys	Pro	Glu	Cys	Tyr	Phe	Glu	Arg	Phe	Ser	Pro	Arg	Cys	Gly	Phe	260	265	270
Cys	Asn	Gln	Pro	Ile	Arg	His	Lys	Met	Val	Thr	Ala	Leu	Gly	Thr	His	275	280	285
Trp	His	Pro	Glu	His	Phe	Cys	Cys	Val	Ser	Cys	Gly	Glu	Pro	Phe	Gly	290	295	300
Asp	Glu	Gly	Phe	His	Glu	Arg	Glu	Gly	Arg	Pro	Tyr	Cys	Arg	Arg	Asp	305	310	315
Phe	Leu	Gln	Leu	Phe	Ala	Pro	Arg	Cys	Gln	Gly	Cys	Gln	Gly	Pro	Ile	325	330	335
Leu	Asp	Asn	Tyr	Ile	Ser	Ala	Leu	Ser	Leu	Leu	Trp	His	Pro	Asp	Cys	340	345	350
Phe	Val	Cys	Arg	Glu	Cys	Phe	Ala	Pro	Phe	Ser	Gly	Gly	Ser	Phe	Phe	355	360	365
Glu	His	Glu	Gly	Arg	Pro	Leu	Cys	Glu	Asn	His	Phe	His	Ala	Arg	Arg	370	375	380
Gly	Ser	Leu	Cys	Pro	Thr	Cys	Gly	Leu	Pro	Val	Thr	Gly	Arg	Cys	Val	385	390	395
Ser	Ala	Leu	Gly	Arg	Arg	Phe	His	Pro	Asp	His	Phe	Ala	Cys	Thr	Phe	405	410	415
Cys	Leu	Arg	Pro	Leu	Thr	Lys	Gly	Ser	Phe	Gln	Glu	Arg	Ala	Gly	Lys	420	425	430
Pro	Tyr	Cys	Gln	Pro	Cys	Phe	Leu	Lys	Leu	Phe	Gly					435	440	

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 <222> (1)...(24)



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                1                      5

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Gln Phe Lys Leu Val Leu Val Gly Asp Gly Gly Thr Gly Lys Thr Thr
  10                      15                      20                      25

ttc gtg aaa cgt cat ttg act ggt gaa ttt gag aag aag tat gta gcc      147
Phe Val Lys Arg His Leu Thr Gly Glu Phe Glu Lys Lys Tyr Val Ala
                30                      35                      40

acc ttg ggt gtt gag gtt cat ccc cta gtg ttc cac acc aac aga gga      195
Thr Leu Gly Val Glu Val His Pro Leu Val Phe His Thr Asn Arg Gly
                45                      50                      55

cct att aag ttc aat gta tgg gac aca gcc ggc cag gag aaa ttc ggt      243
Pro Ile Lys Phe Asn Val Trp Asp Thr Ala Gly Gln Glu Lys Phe Gly
                60                      65                      70

gga ctg aga gat ggc tat tat atc caa gcc cag tgt gcc atc ata atg      291
Gly Leu Arg Asp Gly Tyr Tyr Ile Gln Ala Gln Cys Ala Ile Ile Met
  75                      80                      85

ttt gat gta aca tcg aga gtt act tac aag aat gtg cct aac tgg cat      339
Phe Asp Val Thr Ser Arg Val Thr Tyr Lys Asn Val Pro Asn Trp His
  90                      95                      100                      105

aga gat ctg gta cga gtg tgt gaa aac atc ccc att gtg ttg tgt ggc      387
Arg Asp Leu Val Arg Val Cys Glu Asn Ile Pro Ile Val Leu Cys Gly
                110                      115                      120

aac aaa gtg gat att aag gac agg aaa gtg aag gcg aaa tcc att gtc      435
Asn Lys Val Asp Ile Lys Asp Arg Lys Val Lys Ala Lys Ser Ile Val
                125                      130                      135

ttc cac cga aag aag aat ctt cag tac tac gac att tct gcc aaa agt      483
Phe His Arg Lys Lys Asn Leu Gln Tyr Tyr Asp Ile Ser Ala Lys Ser
                140                      145                      150

aac tac aac ttt gaa aag ccc ttc ctc tgg ctt gct agg aag ctc att      531
Asn Tyr Asn Phe Glu Lys Pro Phe Leu Trp Leu Ala Arg Lys Leu Ile
                155                      160                      165

gga gac cct aac ttg gaa ttt gtt gcc atg cct gct ctc gcc cca cca      579
Gly Asp Pro Asn Leu Glu Phe Val Ala Met Pro Ala Leu Ala Pro Pro
  170                      175                      180                      185

gaa gtt gtc atg gac cca gct ttg gca gca cag tat gag cac gac tta      627
Glu Val Val Met Asp Pro Ala Leu Ala Ala Gln Tyr Glu His Asp Leu
                190                      195                      200

gag gtt gct cag aca act gct ctc ccg gat gag gat gat gac ctg tga      675
Glu Val Ala Gln Thr Thr Ala Leu Pro Asp Glu Asp Asp Asp Leu
                205                      210                      215

gaatgaagct ggagcccagc gtcagaagtc tagttttata ggacagctgtc ctgtgatgtc      735
agcgggtgcag cgtgtgtgcc acctcattat tatctagcta agcgggaacat gtgctttatc      795
tgtgggatgc tgaaggagat gagtgggctt cggagtgaat gtggcagttt aaaaaataac      855

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ttcattgttt ggacctgcat atttagctgt ttggacgcag ttgattcctt gagtttcata 915
tataagactg ctgcagtcac atcacaaatat tcagtgggtga aatcttggtt gttactgtca 975
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actcatccct tggtttataaa tagcattttg aaaccactaa agtagggaag ttttatgccca 1095
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tccctatggt tattttttgta catttgagcc atgtcacaca aactgatgat gacagggtcag 1215
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cagtgtttgc tccaccttca tattggctag gtaggggtcac ctagggaagc acttgctcaa 1335
aatctgtgac ctgtcagaat aaaaatgtgg tttgtacata tcaaatagat attttaaggg 1395
taatatatttc ttttatggca aaagtaataca tgttttaatt tagaacctca aacaggatgg 1455
aacatcagtg gatggcagga ggttggaat tcttgctgtt aaaaataatt acaaattttg 1515
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<210> 6  
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 <212> PRT  
 <213> Homo sapien

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Met Ala Ala Gln Gly Glu Pro Gln Val Gln Phe Lys Leu Val Leu Val
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Gly Asp Gly Gly Thr Gly Lys Thr Thr Phe Val Lys Arg His Leu Thr
20          25          30
Gly Glu Phe Glu Lys Lys Tyr Val Ala Thr Leu Gly Val Glu Val His
35          40          45
Pro Leu Val Phe His Thr Asn Arg Gly Pro Ile Lys Phe Asn Val Trp
50          55          60
Asp Thr Ala Gly Gln Glu Lys Phe Gly Gly Leu Arg Asp Gly Tyr Tyr
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Val Ala Met Pro Ala Leu Ala Pro Pro Glu Val Val Met Asp Pro Ala
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Thr Ala Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro	
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<213> Homo sapien

<400> 8

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Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys
65          70          75          80
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85          90          95
Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu Asp Glu
100         105         110
Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile Ser Val
115         120         125
His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val
130         135         140
Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala
145         150         155         160
Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln
165         170         175
Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys
180         185         190
Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met
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<213> Homo sapien

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<221> VARIANT

<222> 2-3, 5-13, 15, 17-18, 20-21, 23-28, 30-31

<223> Xaa can be any amino acid

<400> 11

Cys	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	His
1				5					10						15	
Xaa	Xaa	Cys	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Cys
			20					25						30		

<210> 12

<211> 50

<212> PRT

<213> Homo sapien

<220>

<221> VARIANT

<222> 2-3, 5-20, 22-23, 25-26, 28-29, 31-46, 48-49

<223> Xaa can be any amino acid

<400> 12

Cys	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5					10					15		
Xaa	Xaa	Xaa	Xaa	His	Xaa	Xaa	Cys	Xaa	Xaa	Cys	Xaa	Xaa	Cys	Xaa	Xaa	
			20					25					30			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	
			35				40						45			
Xaa	Cys															
	50															

<210> 13

<211> 1497

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 13

ctgcagcttg	ttctttaatg	tcaggagact	ctcccttctg	cttgctcctgg	tgggccctgg	60
ggggagcggg	gagggaatac	ctaagagcaa	ttggtagctg	gtacttctaa	tgcctcttcc	120
tctccaacc	tccaagagtc	tgttttggga	ttgggttcag	gaatgaaatt	ctgcctgtgc	180
taacctcctg	gggagccggt	agacttgtct	gttaaaaatc	gcttctgctt	ttggagccta	240
aagcccgggt	ccgaaaaaca	agtggtatct	aggggaaaga	ggggtcttca	aaggctacag	300
tgagtcattc	cagccttcaa	ccatactacg	ccagcactac	gttctctaaa	gccactctgc	360
gctagcttgc	ggtgagggga	ggggagaaaa	ggaaagggga	ggggagggga	ggggagggag	420
aaaggagggtg	ggaaggcaga	gaggccggct	gcgggggcgg	gaccgactca	caaactgttc	480
gatttcggtt	ccacctccca	gcgccccctc	ggagatccct	aggagccagc	ctgctgggag	540
aaccagaggg	tccggagcaa	acctggaggc	tgagagggca	tcagagggga	aaagactgag	600
ctagccactc	cagtgccata	cagaagctta	agggacgcac	cacgccagcc	ccagcccagc	660
gacagccaac	gcctgttgca	gagcggcggc	ttcgaagccg	ccgcccagga	gctgcccttt	720
cctcttcggt	gaagtctcta	aaagctgcgg	gagactcaga	ggaagcaagg	aaagtgtccg	780
gtaggactac	ggctgccttt	gtcctcttcc	cctctaccct	tacccctctc	tgggtcccct	840
ctccaggagc	tgactaggca	ggctttcttg	ccaacctctt	cccctacacc	cccagctctg	900
ccagccagtt	tgcacagagg	taaactccct	ttggctgaga	gtaggggagc	ttgttgaca	960
ttgcaaggaa	ggcttttgga	agcccagaga	ctgaggagca	acagcacgcc	caggagagtc	1020
cctggttcca	ggttctcgcc	cctgcacctc	ctcctgcccg	cccctcacc	tgtgtgtggt	1080
gttagaaatg	aaaagatgaa	aaggcagcta	gggtttcagt	agtcgaaagc	aaaacaaaag	1140
ctaaaagaaa	acaaaaagaa	aatagcccag	ttcttatctg	cacctgcttc	agtggacttt	1200
gaatttgga	ggcagaggat	ttcccccttt	ccctcccgtc	aaggtttgag	catcttttaa	1260

tctgttcttc	aagtatttag	agacaaactg	tgtaagtagc	agggcagatc	ctgtcttgcg	1320
cggtgccttcc	tttactggag	actttgaggt	tatctgggca	ctccccccac	ccaccccccc	1380
tcttgcaagt	tttcttcccc	ggagcttccc	gcaggtgggc	agctagctgc	agatactaca	1440
tcatcagtca	ggagaactct	tcagagcaag	agacgaggag	gcaggataag	ggaattc	1497

<210> 14

<211> 600

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 14

ctgcagcttg	ttctttaatg	tcaggagact	ctcccttctg	cttgtcctgg	tgggccctgg	60
ggggagcggg	gaggaatac	ctaagagcaa	ttggtagctg	gtacttctaa	tgccctcttc	120
tcctccaacc	tccaagagtc	tgttttggga	ttgggttcag	gaatgaaatt	ctgcctgtgc	180
taacctcctg	gggagccggt	agacttgtct	gttaaaaaatc	gcttctgctt	ttggagccta	240
aagcccggtt	ccgaaaaaca	agtggatatt	aggggaaaga	ggggtcttca	aaggctacag	300
tgagtcattc	cagccttcaa	ccatactacg	ccagcactac	gttctctaaa	gccactctgc	360
ctaagcttgc	ggtgagggga	ggggagaaaa	ggaaagggga	ggggagggga	ggggagggag	420
aaaggaggtg	ggaaggcaga	gaggccggct	gcggggggcg	gaccgactca	caaaactgtc	480
gatttcggtt	ccacctccca	gcgccccctc	ggagatccct	aggagccagc	ctgctgggag	540
aaccagaggg	tccggagcaa	acctggaggc	tgagagggca	tcagagggga	aaagactgag	600

<210> 15

<211> 359

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 15

cccaagcgct	agtgttctgt	tctctttttg	taatottgga	atctttttgtt	gctctaaata	60
caattaaaaa	tggcagaaac	ttgtttgttg	gaatacatgt	gtgactcttg	gtttgtctct	120
gcgtctgggt	ttagaaatgt	catccattgt	gtaaaatact	ggcttggttg	tctgccagct	180
aaaacttgcc	acagcccctg	ttgtgactgc	aggctcaagt	tattgttaac	aaagagcccc	240
aagaaaagct	gctaattgtc	tcttatcacc	attgttaatt	tgtaaaaaca	taaaacaatc	300
taaaatttca	gatgaatgtc	atcagagttc	ttttcattag	ctctttttat	tggtgtct	359

<210> 16

<211> 899

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 16

Met	Glu	Val	Gln	Leu	Gly	Leu	Gly	Arg	Val	Tyr	Pro	Arg	Pro	Pro	Ser
1			5					10						15	
Lys	Thr	Tyr	Arg	Gly	Ala	Phe	Gln	Asn	Leu	Phe	Gln	Ser	Val	Arg	Glu
			20					25					30		
Ala	Ile	Gln	Asn	Pro	Gly	Pro	Arg	His	Pro	Glu	Ala	Ala	Asn	Ile	Ala
			35					40					45		
Pro	Pro	Gly	Ala	Cys	Leu	Gln	Gln	Arg	Gln	Glu	Thr	Ser	Pro	Arg	Arg
			50				55						60		

Arg	Arg	Arg	Gln	Gln	His	Thr	Glu	Asp	Gly	Ser	Pro	Gln	Ala	His	Ile
65					70					75					80
Arg	Gly	Pro	Thr	Gly	Tyr	Leu	Ala	Leu	Glu	Glu	Gln	Gln	Pro	Ser	
				85					90					95	
Gln	Gln	Gln	Ala	Ala	Ser	Glu	Gly	His	Pro	Glu	Ser	Ser	Cys	Leu	Pro
			100					105					110		
Glu	Pro	Gly	Ala	Ala	Thr	Ala	Pro	Gly	Lys	Gly	Leu	Pro	Gln	Gln	Pro
		115					120					125			
Pro	Ala	Pro	Pro	Asp	Gln	Asp	Asp	Ser	Ala	Ala	Pro	Ser	Thr	Leu	Ser
	130					135					140				
Leu	Leu	Gly	Pro	Thr	Phe	Pro	Gly	Leu	Ser	Ser	Cys	Ser	Ala	Asp	Ile
145					150					155					160
Lys	Asp	Ile	Leu	Asn	Glu	Ala	Gly	Thr	Met	Gln	Leu	Leu	Gln	Gln	Gln
				165					170					175	
Gln	Gln	Gln	Gln	Gln	His	Gln	Gln	Gln	His	Gln	Gln	His	Gln	Gln	Gln
			180					185					190		
Gln	Glu	Val	Ile	Ser	Glu	Gly	Ser	Ser	Ala	Arg	Ala	Arg	Glu	Ala	Thr
		195					200					205			
Gly	Ala	Pro	Ser	Ser	Ser	Lys	Asp	Ser	Tyr	Leu	Gly	Gly	Asn	Ser	Thr
	210					215					220				
Ile	Ser	Asp	Ser	Ala	Lys	Glu	Leu	Cys	Lys	Ala	Val	Ser	Val	Ser	Met
225					230					235					240
Gly	Leu	Gly	Val	Glu	Ala	Leu	Glu	His	Leu	Ser	Pro	Gly	Glu	Gln	Leu
				245					250					255	
Arg	Gly	Asp	Cys	Met	Tyr	Ala	Ser	Leu	Leu	Gly	Gly	Pro	Pro	Ala	Val
			260					265					270		
Arg	Pro	Thr	Pro	Cys	Ala	Pro	Leu	Pro	Glu	Cys	Lys	Gly	Leu	Pro	Leu
		275					280					285			
Asp	Glu	Gly	Pro	Gly	Lys	Ser	Thr	Glu	Glu	Thr	Ala	Glu	Tyr	Ser	Ser
	290					295					300				
Phe	Lys	Gly	Gly	Tyr	Ala	Lys	Gly	Leu	Glu	Gly	Glu	Ser	Leu	Gly	Cys
305					310					315					320
Ser	Gly	Ser	Ser	Glu	Ala	Gly	Ser	Ser	Gly	Thr	Leu	Glu	Ile	Pro	Ser
				325					330					335	
Ser	Leu	Ser	Leu	Tyr	Lys	Ser	Gly	Ala	Leu	Asp	Glu	Ala	Ala	Ala	Tyr
			340					345					350		
Gln	Asn	Arg	Asp	Tyr	Tyr	Asn	Phe	Pro	Leu	Ala	Leu	Ser	Gly	Pro	Pro
	355						360					365			
His	Pro	Pro	Pro	Pro	Thr	His	Pro	His	Ala	Arg	Ile	Lys	Leu	Glu	Asn
	370					375					380				
Pro	Leu	Asp	Tyr	Gly	Ser	Ala	Trp	Ala	Ala	Ala	Ala	Ala	Gln	Cys	Arg
385					390					395					400
Tyr	Gly	Asp	Leu	Gly	Ser	Leu	His	Gly	Gly	Ser	Val	Ala	Gly	Pro	Ser
				405					410					415	
Thr	Gly	Ser	Pro	Pro	Ala	Thr	Thr	Ser	Ser	Ser	Trp	His	Thr	Leu	Phe
			420					425					430		
Thr	Ala	Glu	Gly	Gln	Leu	Tyr	Gly	Pro	Gly	Gly	Gly	Gly	Gly	Gly	Ser
		435					440					445			
Ser	Ser	Pro	Ser	Asp	Ala	Gly	Pro	Val	Ala	Pro	Tyr	Gly	Tyr	Thr	Arg
	450					455					460				
Pro	Pro	Gln	Gly	Leu	Thr	Ser	Gln	Glu	Ser	Asp	Tyr	Ser	Ala	Ser	Glu
465					470					475					480
Val	Trp	Tyr	Pro	Gly	Gly	Val	Val	Asn	Arg	Val	Pro	Tyr	Pro	Ser	Pro
				485					490					495	
Asn	Cys	Val	Lys	Ser	Glu	Met	Gly	Pro	Trp	Met	Glu	Asn	Tyr	Ser	Gly
			500					505					510		
Pro	Tyr	Gly	Asp	Met	Arg	Leu	Asp	Ser	Thr	Arg	Asp	His	Val	Leu	Pro
		515					520					525			
Ile	Asp	Tyr	Tyr	Phe	Pro	Pro	Gln	Lys	Thr	Cys	Leu	Ile	Cys	Gly	Asp
	530					535					540				

Glu	Ala	Ser	Gly	Cys	His	Tyr	Gly	Ala	Leu	Thr	Cys	Gly	Ser	Cys	Lys
545					550					555					560
Val	Phe	Phe	Lys	Arg	Ala	Ala	Glu	Gly	Lys	Gln	Lys	Tyr	Leu	Cys	Ala
				565					570					575	
Ser	Arg	Asn	Asp	Cys	Thr	Ile	Asp	Lys	Phe	Arg	Arg	Lys	Asn	Cys	Pro
			580					585					590		
Ser	Cys	Arg	Leu	Arg	Lys	Cys	Tyr	Glu	Ala	Gly	Met	Thr	Leu	Gly	Ala
		595					600					605			
Arg	Lys	Leu	Lys	Lys	Leu	Gly	Asn	Leu	Lys	Leu	Gln	Glu	Glu	Gly	Glu
610						615					620				
Asn	Ser	Asn	Ala	Gly	Ser	Pro	Thr	Glu	Asp	Pro	Ser	Gln	Lys	Met	Thr
625					630					635					640
Val	Ser	His	Ile	Glu	Gly	Tyr	Glu	Cys	Gln	Pro	Ile	Phe	Leu	Asn	Val
			645						650					655	
Leu	Glu	Ala	Ile	Glu	Pro	Gly	Val	Val	Cys	Ala	Gly	His	Asp	Asn	Asn
			660					665					670		
Gln	Pro	Asp	Ser	Phe	Ala	Ala	Leu	Leu	Ser	Ser	Leu	Asn	Glu	Leu	Gly
		675					680					685			
Glu	Arg	Gln	Leu	Val	His	Val	Val	Lys	Trp	Ala	Lys	Ala	Leu	Pro	Gly
690						695					700				
Phe	Arg	Asn	Leu	His	Val	Asp	Asp	Gln	Met	Ala	Val	Ile	Gln	Tyr	Ser
705					710					715					720
Trp	Met	Gly	Leu	Met	Val	Phe	Ala	Met	Gly	Trp	Arg	Ser	Phe	Thr	Asn
			725						730					735	
Val	Asn	Ser	Arg	Met	Leu	Tyr	Phe	Ala	Pro	Asp	Leu	Val	Phe	Asn	Glu
			740					745					750		
Tyr	Arg	Met	His	Lys	Ser	Arg	Met	Tyr	Ser	Gln	Cys	Val	Arg	Met	Arg
		755					760					765			
His	Leu	Ser	Gln	Glu	Phe	Gly	Trp	Leu	Gln	Ile	Thr	Pro	Gln	Glu	Phe
770						775					780				
Leu	Cys	Met	Lys	Ala	Leu	Leu	Phe	Ser	Ile	Ile	Pro	Val	Asp	Gly	
785					790				795					800	
Leu	Lys	Asn	Gln	Lys	Phe	Phe	Asp	Glu	Leu	Arg	Met	Asn	Tyr	Ile	Lys
			805						810					815	
Glu	Leu	Asp	Arg	Ile	Ile	Ala	Cys	Lys	Arg	Lys	Asn	Pro	Thr	Ser	Cys
			820					825					830		
Ser	Arg	Arg	Phe	Tyr	Gln	Leu	Thr	Lys	Leu	Leu	Asp	Ser	Val	Gln	Pro
		835					840					845			
Ile	Ala	Arg	Glu	Leu	His	Gln	Phe	Thr	Phe	Asp	Leu	Leu	Ile	Lys	Ser
850						855					860				
His	Met	Val	Ser	Val	Asp	Phe	Pro	Glu	Met	Met	Ala	Glu	Ile	Ile	Ser
865					870					875					880
Val	Gln	Val	Pro	Lys	Ile	Leu	Ser	Gly	Lys	Val	Lys	Pro	Ile	Tyr	Phe
				885					890					895	

His Thr Gln

<210> 17

<211> 2988

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 17

gcttcccgcga	ggtggggcagc	tagctgcaga	tactacatca	tcagtcagga	gaactcttca	60
gagcaagaga	cgaggaggca	ggataaggga	attcggtgga	agctacagac	aagctcaagg	120
atggaggtgc	agttagggct	gggaagggtc	tacccacggc	ccccatccaa	gacctatcga	180
ggagcgttcc	agaatctgtt	ccagagcgtg	cgcgaaagcga	tccagaaccc	gggccccagg	240

caccctgagg	ccgctaacat	agcacctccc	ggcgccctggt	tacagcagag	gcaggagact	300
agcccccggc	ggcggcggcg	gcagcagcac	actgaggatg	gttctcctca	agccccacatc	360
agaggcccca	caggctacct	ggccctggag	gaggaacagc	agccttcaca	gcagcaggca	420
gcctccgagg	gccaccctga	gagcagctgc	ctccccgagc	ctggggcggc	caccgctcct	480
ggcaaggggc	tgccgcagca	gccaccagct	cctccagatc	aggatgactc	agctgccccca	540
tccacgttgt	ccctgctggg	ccccactttc	ccaggcttaa	gcagctgctc	cgccgacatt	600
aaagacattt	tgaacgaggc	cggcaccatg	caacttcttc	agcagcagca	acaacagcag	660
cagcaccaac	agcagcacca	acagcaccaa	cagcagcagg	aggtaatctc	cgaaggcagc	720
agcgcaagag	ccaggggaggc	cacgggggct	ccctcttcct	ccaaggatag	ttacctaggg	780
ggcaattcaa	ccatatctga	cagtgccaa	gagttgtgta	aagcagtgctc	tgtgtccatg	840
ggattgggtg	tggaaagcatt	ggaacatctg	agtccagggg	aacagcttcg	gggagactgc	900
atgtacgcgt	cgctcctggg	aggtccaccc	gcggtgcgtc	ccactccttg	tgcgccgctg	960
ccggaatgca	aaggtcttcc	cctggacgaa	ggcccaggca	aaagcactga	agagactgct	1020
gagtattcct	ctttcaaggg	aggttacgcc	aaaggattgg	aaggtgagag	cttgggggtgc	1080
tctggcagca	gtgaagcagg	tagctctggg	acacttgaga	tcccgtcctc	tctgtctctg	1140
tataaatctg	gagcactaga	cgaggcagca	gcataccaga	atcgcgacta	ctacaacttt	1200
ccgctggctc	tgtccggggc	gccgcacccc	ccgcccccta	cccatccaca	cgcccgtatc	1260
aaagctggaga	accatttggg	ctacggcagc	gcctgggctg	cggcggcagc	gcaatgccgc	1320
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ccagccacca	cctcttcttc	ctggcatact	ctcttcacag	ctgaagaagg	ccaattatat	1440
gggcccaggag	gcgggggagg	cagcagcagc	ccaagcgatg	ccgggcctgt	agccccctat	1500
ggctacactc	ggccccctca	ggggctgaca	agccaggaga	gtgactactc	tgccctccgaa	1560
gtgtgggtatc	ctggtggagt	tgtgaacaga	gtaccctatc	ccagtcccaa	ttgtgtcaaa	1620
agtgaatatg	gaccttggat	ggagaactac	tccggacctt	atggggacat	gcgtttggac	1680
agtaccaggg	accatgtttt	acccatcgac	tattactttc	caccccagaa	gacctgcctg	1740
atctgtggag	atgaagcttc	tggctgtcac	tacggagctc	tcacttgtgg	cagctgcaag	1800
gtcttcttca	aaagagccgc	tgaagggaaa	cagaagtatc	tatgtgccag	cagaaacgat	1860
tgtaccattg	ataaatttcg	gaggaaaaat	tgcccactct	gtcgtctccg	gaaatgttat	1920
gaagcagggg	tgactctggg	agctcgtaag	ctgaagaaac	ttggaaatct	aaaactacag	1980
gaggaaggag	aaaactccaa	tgctggcagc	cccactgagg	acccatccca	gaagatgact	2040
gtatcacaca	ttgaaggcta	tgaatgtcag	cctatctttc	ttaacgtcct	ggaagccatt	2100
gagccaggag	tgggtgtgtg	cggacatgac	aacaaccaac	cagattcctt	tgctgccttg	2160
ttatctagcc	tcaatgagct	tggagagagg	cagcttgtgc	atgtggtcaa	gtgggccaag	2220
gccttgccctg	gcttccgcaa	cttgcattgt	gatgaccaga	tggcggtcat	tcagtattcc	2280
tggatgggac	tgatgggtatt	tgccatgggt	tggcggtcct	tcactaatgt	caactccagg	2340
atgctctact	ttgcacctga	cttggttttc	aatgagtacc	gcatgcacaa	gtctcgatg	2400
tacagccagt	gtgtgaggat	gaggcacctg	tctcaagagt	ttggatggct	ccaaataacc	2460
ccccaggaat	tcctgtgcat	gaaagcactg	ctgctcttca	gcattattcc	agtggatggg	2520
ctgaaaaatc	aaaaattctt	tgatgaactt	cgaatgaact	acatcaagga	actcgatcgc	2580
atcattgcct	gcaaaagaaa	gaatcccaca	tcctgctcaa	ggcgcttcta	ccagctcacc	2640
aagctccttg	attctgtgca	gcctattgca	agagagctgc	atcagttcac	ttttgacctg	2700
ctaatacaagt	cccatatggg	gagcgtggac	tttctgaaa	tgatggcaga	gatcatctct	2760
gtgcaagtgc	ccaagatcct	ttctgggaaa	gtcaagccca	tctatttcca	cacacagtga	2820
agatttggaa	accctaatac	ccaaaaccca	ccttggtccc	tttccagatg	tcttctgcct	2880
gttatataac	tctgcactac	ttctctgcag	tgcttggggg	gaaattcctc	tactgatgta	2940
cagtcagacg	tgaacagggt	cctcagttct	atttctctgg	cttctcct		2988

<210> 18

<211> 899

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 18

Met	Glu	Val	Gln	Leu	Gly	Leu	Gly	Arg	Val	Tyr	Pro	Arg	Pro	Pro	Ser
1				5				10						15	
Lys	Thr	Tyr	Arg	Gly	Ala	Phe	Gln	Asn	Leu	Phe	Gln	Ser	Val	Arg	Glu
			20					25						30	

Ala	Ile	Gln	Asn	Pro	Gly	Pro	Arg	His	Pro	Glu	Ala	Ala	Asn	Ile	Ala
	35					40					45				
Pro	Pro	Gly	Ala	Cys	Leu	Gln	Gln	Arg	Gln	Glu	Thr	Ser	Pro	Arg	Arg
	50					55				60					
Arg	Arg	Arg	Gln	Gln	His	Thr	Glu	Asp	Gly	Ser	Pro	Gln	Ala	His	Ile
65					70					75					80
Arg	Gly	Pro	Thr	Gly	Tyr	Leu	Ala	Leu	Glu	Glu	Glu	Gln	Gln	Pro	Ser
				85					90					95	
Gln	Gln	Gln	Ala	Ala	Ser	Glu	Gly	His	Pro	Glu	Ser	Ser	Cys	Leu	Pro
			100					105					110		
Glu	Pro	Gly	Ala	Ala	Thr	Ala	Pro	Gly	Lys	Gly	Leu	Pro	Gln	Gln	Pro
		115					120					125			
Pro	Ala	Pro	Pro	Asp	Gln	Asp	Asp	Ser	Ala	Ala	Pro	Ser	Thr	Leu	Ser
	130					135					140				
Leu	Leu	Gly	Pro	Thr	Phe	Pro	Gly	Leu	Ser	Ser	Cys	Ser	Ala	Asp	Ile
145					150					155					160
Lys	Asp	Ile	Leu	Asn	Glu	Ala	Gly	Thr	Met	Gln	Leu	Leu	Gln	Gln	Gln
				165					170					175	
Gln	Gln	Gln	Gln	Gln	His	Gln	Gln	Gln	His	Gln	Gln	His	Gln	Gln	Gln
			180					185					190		
Gln	Glu	Val	Ile	Ser	Glu	Gly	Ser	Ser	Ala	Arg	Ala	Arg	Glu	Ala	Thr
	195						200					205			
Gly	Ala	Pro	Ser	Ser	Ser	Lys	Asp	Ser	Tyr	Leu	Gly	Gly	Asn	Ser	Thr
	210					215					220				
Ile	Ser	Asp	Ser	Ala	Lys	Glu	Leu	Cys	Lys	Ala	Val	Ser	Val	Ser	Met
225					230					235					240
Gly	Leu	Gly	Val	Glu	Ala	Leu	Glu	His	Leu	Ser	Pro	Gly	Glu	Gln	Leu
				245					250					255	
Arg	Gly	Asp	Cys	Met	Tyr	Ala	Ser	Leu	Leu	Gly	Gly	Pro	Pro	Ala	Val
			260				265					270			
Arg	Pro	Thr	Pro	Cys	Ala	Pro	Leu	Pro	Glu	Cys	Lys	Gly	Leu	Pro	Leu
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Asp	Glu	Gly	Pro	Gly	Lys	Ser	Thr	Glu	Glu	Thr	Ala	Glu	Tyr	Ser	Ser
	290				295						300				
Phe	Lys	Gly	Gly	Tyr	Ala	Lys	Gly	Leu	Glu	Gly	Glu	Ser	Leu	Gly	Cys
305					310					315					320
Ser	Gly	Ser	Ser	Glu	Ala	Gly	Ser	Ser	Gly	Thr	Leu	Glu	Ile	Pro	Ser
				325					330					335	
Ser	Leu	Ser	Leu	Tyr	Lys	Ser	Gly	Ala	Leu	Asp	Glu	Ala	Ala	Ala	Tyr
			340				345					350			
Gln	Asn	Arg	Asp	Tyr	Tyr	Asn	Phe	Pro	Leu	Ala	Leu	Ser	Gly	Pro	Pro
	355						360					365			
His	Pro	Pro	Pro	Pro	Thr	His	Pro	His	Ala	Arg	Ile	Lys	Leu	Glu	Asn
	370				375						380				
Pro	Leu	Asp	Tyr	Gly	Ser	Ala	Trp	Ala	Ala	Ala	Ala	Ala	Gln	Cys	Arg
385					390					395					400
Tyr	Gly	Asp	Leu	Gly	Ser	Leu	His	Gly	Gly	Ser	Val	Ala	Gly	Pro	Ser
				405					410					415	
Thr	Gly	Ser	Pro	Pro	Ala	Thr	Thr	Ser	Ser	Ser	Trp	His	Thr	Leu	Phe
			420					425					430		
Thr	Ala	Glu	Glu	Gly	Gln	Leu	Tyr	Gly	Pro	Gly	Gly	Gly	Gly	Gly	Ser
	435					440					445				
Ser	Ser	Pro	Ser	Asp	Ala	Gly	Pro	Val	Ala	Pro	Tyr	Gly	Tyr	Thr	Arg
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Pro	Pro	Gln	Gly	Leu	Thr	Ser	Gln	Glu	Ser	Asp	Tyr	Ser	Ala	Ser	Glu
465					470					475					480
Val	Trp	Tyr	Pro	Gly	Gly	Val	Val	Asn	Arg	Val	Pro	Tyr	Pro	Ser	Pro
				485					490					495	
Asn	Cys	Val	Lys	Ser	Glu	Met	Gly	Pro	Trp	Met	Glu	Asn	Tyr	Ser	Gly
			500					505					510		

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Pro Tyr Gly Asp Met Arg Leu Asp Ser Thr Arg Asp His Val Leu Pro
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Ile Asp Tyr Tyr Phe Pro Pro Gln Lys Thr Cys Leu Ile Cys Gly Asp
530 535 540
Glu Ala Ser Gly Cys His Tyr Gly Ala Leu Thr Cys Gly Ser Cys Lys
545 550 555 560
Val Phe Phe Lys Arg Ala Ala Glu Gly Lys Gln Lys Tyr Leu Cys Ala
565 570 575
Ser Arg Asn Asp Cys Thr Ile Asp Lys Phe Arg Arg Lys Asn Cys Pro
580 585 590
Ser Cys Arg Leu Arg Lys Cys Tyr Glu Ala Gly Met Thr Leu Gly Ala
595 600 605
Arg Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu Gln Glu Glu Gly Glu
610 615 620
Asn Ser Asn Ala Gly Ser Pro Thr Glu Asp Pro Ser Gln Lys Met Thr
625 630 635 640
Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile Phe Leu Asn Val
645 650 655
Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly His Asp Asn Asn
660 665 670
Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu Asn Glu Leu Gly
675 680 685
Glu Arg Gln Leu Val His Val Val Lys Trp Ala Lys Ala Leu Pro Gly
690 695 700
Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val Ile Gln Tyr Ser
705 710 715 720
Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg Ser Phe Thr Asn
725 730 735
Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu Val Phe Asn Glu
740 745 750
Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys Val Arg Met Arg
755 760 765
His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr Pro Gln Glu Phe
770 775 780
Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile Pro Val Asp Gly
785 790 795 800
Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met Asn Tyr Ile Lys
805 810 815
Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn Pro Thr Ser Cys
820 825 830
Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Val Gln Pro
835 840 845
Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu Leu Ile Lys Ser
850 855 860
His Met Val Ser Val Asp Phe Pro Glu Met Met Ala Glu Ile Ile Ser
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Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys Pro Ile Tyr Phe
885 890 895
His Thr Gln

```

<210> 19

<211> 2988

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 19



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<210> 20

<211> 899

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 20

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Lys	Thr	Tyr	Arg	Gly	Ala	Phe	Gln	Asn	Leu	Phe	Gln	Ser	Val	Arg	Glu	20	25	30	
Ala	Ile	Gln	Asn	Pro	Gly	Pro	Arg	His	Pro	Glu	Ala	Ala	Asn	Ile	Ala	35	40	45	
Pro	Pro	Gly	Ala	Cys	Leu	Gln	Gln	Arg	Gln	Glu	Thr	Ser	Pro	Arg	Arg	50	55	60	
Arg	Arg	Arg	Gln	Gln	His	Thr	Glu	Asp	Gly	Ser	Pro	Gln	Ala	His	Ile	65	70	75	80
Arg	Gly	Pro	Thr	Gly	Tyr	Leu	Ala	Leu	Glu	Glu	Gln	Gln	Pro	Ser		85	90	95	
Gln	Gln	Gln	Ala	Ala	Ser	Glu	Gly	His	Pro	Glu	Ser	Ser	Cys	Leu	Pro	100	105	110	
Glu	Pro	Gly	Ala	Ala	Thr	Ala	Pro	Gly	Lys	Gly	Leu	Pro	Gln	Gln	Pro	115	120	125	
Pro	Ala	Pro	Pro	Asp	Gln	Asp	Asp	Ser	Ala	Ala	Pro	Ser	Thr	Leu	Ser	130	135	140	
Leu	Leu	Gly	Pro	Thr	Phe	Pro	Gly	Leu	Ser	Ser	Cys	Ser	Ala	Asp	Ile	145	150	155	160
Lys	Asp	Ile	Leu	Asn	Glu	Ala	Gly	Thr	Met	Gln	Leu	Leu	Gln	Gln	Gln	165	170	175	
Gln	Gln	Gln	Gln	Gln	His	Gln	Gln	Gln	His	Gln	Gln	His	Gln	Gln	Gln	180	185	190	
Gln	Glu	Val	Ile	Ser	Glu	Gly	Ser	Ser	Ala	Arg	Ala	Arg	Glu	Ala	Thr	195	200	205	
Gly	Ala	Pro	Ser	Ser	Ser	Lys	Asp	Ser	Tyr	Leu	Gly	Gly	Asn	Ser	Thr	210	215	220	
Ile	Ser	Asp	Ser	Ala	Lys	Glu	Leu	Cys	Lys	Ala	Val	Ser	Val	Ser	Met	225	230	235	240
Gly	Leu	Gly	Val	Glu	Ala	Leu	Glu	His	Leu	Ser	Pro	Gly	Glu	Gln	Leu	245	250	255	
Arg	Gly	Asp	Cys	Met	Tyr	Ala	Ser	Leu	Leu	Gly	Gly	Pro	Pro	Ala	Val	260	265	270	
Arg	Pro	Thr	Pro	Cys	Ala	Pro	Leu	Pro	Glu	Cys	Lys	Gly	Leu	Pro	Leu	275	280	285	
Asp	Glu	Gly	Pro	Gly	Lys	Ser	Thr	Glu	Glu	Thr	Ala	Glu	Tyr	Ser	Ser	290	295	300	
Phe	Lys	Gly	Gly	Tyr	Ala	Lys	Gly	Leu	Glu	Gly	Glu	Ser	Leu	Gly	Cys	305	310	315	320
Ser	Gly	Ser	Ser	Glu	Ala	Gly	Ser	Ser	Gly	Thr	Leu	Glu	Ile	Pro	Ser	325	330	335	
Ser	Leu	Ser	Leu	Tyr	Lys	Ser	Gly	Ala	Leu	Asp	Glu	Ala	Ala	Ala	Tyr	340	345	350	
Gln	Asn	Arg	Asp	Tyr	Tyr	Asn	Phe	Pro	Leu	Ala	Leu	Ser	Gly	Pro	Pro	355	360	365	
His	Pro	Pro	Pro	Pro	Thr	His	Pro	His	Ala	Arg	Ile	Lys	Leu	Glu	Asn	370	375	380	
Pro	Leu	Asp	Tyr	Gly	Ser	Ala	Trp	Ala	Ala	Ala	Ala	Gln	Cys	Arg		385	390	395	400
Tyr	Gly	Asp	Leu	Gly	Ser	Leu	His	Gly	Gly	Ser	Val	Ala	Gly	Pro	Ser	405	410	415	
Thr	Gly	Ser	Pro	Pro	Ala	Thr	Thr	Ser	Ser	Ser	Trp	His	Thr	Leu	Phe	420	425	430	
Thr	Ala	Glu	Glu	Gly	Gln	Leu	Tyr	Gly	Pro	Gly	Gly	Gly	Gly	Gly	Ser	435	440	445	
Ser	Ser	Pro	Ser	Asp	Ala	Gly	Pro	Val	Ala	Pro	Tyr	Gly	Tyr	Thr	Arg	450	455	460	
Pro	Pro	Gln	Gly	Leu	Thr	Ser	Gln	Glu	Ser	Asp	Tyr	Ser	Ala	Ser	Glu	465	470	475	480

Val	Trp	Tyr	Pro	Gly	Gly	Val	Val	Asn	Arg	Val	Pro	Tyr	Pro	Ser	Pro		
				485					490					495			
Asn	Cys	Val	Lys	Ser	Glu	Met	Gly	Pro	Trp	Met	Glu	Asn	Tyr	Ser	Gly		
			500					505					510				
Pro	Tyr	Gly	Asp	Met	Arg	Leu	Asp	Ser	Thr	Arg	Asp	His	Val	Leu	Pro		
		515					520					525					
Ile	Asp	Tyr	Tyr	Phe	Pro	Pro	Gln	Lys	Thr	Cys	Leu	Ile	Cys	Gly	Asp		
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Glu	Ala	Ser	Gly	Cys	His	Tyr	Gly	Ala	Leu	Thr	Cys	Gly	Ser	Cys	Lys		
545					550					555					560		
Val	Phe	Phe	Lys	Arg	Ala	Ala	Glu	Gly	Lys	Gln	Lys	Tyr	Leu	Cys	Ala		
				565					570					575			
Ser	Arg	Asn	Asp	Cys	Thr	Ile	Asp	Lys	Phe	Arg	Arg	Lys	Asn	Cys	Pro		
			580					585					590				
Ser	Cys	Arg	Leu	Arg	Lys	Cys	Tyr	Glu	Ala	Gly	Met	Thr	Leu	Gly	Ala		
		595					600					605					
Arg	Lys	Leu	Lys	Lys	Leu	Gly	Asn	Leu	Lys	Leu	Gln	Glu	Glu	Gly	Glu		
	610					615					620						
Asn	Ser	Asn	Ala	Gly	Ser	Pro	Thr	Glu	Asp	Pro	Ser	Gln	Lys	Met	Thr		
625					630					635					640		
Val	Ser	His	Ile	Glu	Gly	Tyr	Glu	Cys	Gln	Pro	Ile	Phe	Leu	Asn	Val		
				645					650					655			
Leu	Glu	Ala	Ile	Glu	Pro	Gly	Val	Val	Cys	Ala	Gly	His	Asp	Asn	Asn		
			660					665					670				
Gln	Pro	Asp	Ser	Phe	Ala	Ala	Leu	Leu	Ser	Ser	Leu	Asn	Glu	Leu	Gly		
		675					680					685					
Glu	Arg	Gln	Leu	Val	His	Val	Val	Lys	Trp	Ala	Lys	Ala	Leu	Pro	Gly		
	690					695					700						
Phe	Arg	Asn	Leu	His	Val	Asp	Asp	Gln	Met	Ala	Val	Ile	Gln	Tyr	Ser		
705					710					715					720		
Trp	Met	Gly	Leu	Met	Val	Phe	Ala	Met	Gly	Trp	Arg	Ser	Phe	Thr	Asn		
				725					730					735			
Val	Asn	Ser	Arg	Met	Leu	Tyr	Phe	Ala	Pro	Asp	Leu	Val	Phe	Asn	Glu		
			740					745					750				
Tyr	Arg	Met	His	Lys	Ser	Arg	Met	Tyr	Ser	Gln	Cys	Val	Arg	Met	Arg		
		755					760					765					
His	Leu	Ser	Gln	Glu	Phe	Gly	Trp	Leu	Gln	Ile	Thr	Pro	Gln	Glu	Phe		
	770					775					780						
Leu	Cys	Met	Lys	Ala	Leu	Leu	Phe	Ser	Ile	Ile	Pro	Val	Asp	Gly			
785					790				795					800			
Leu	Lys	Asn	Gln	Lys	Phe	Phe	Asp	Glu	Leu	Arg	Met	Asn	Tyr	Ile	Lys		
			805						810					815			
Glu	Leu	Asp	Arg	Ile	Ile	Ala	Cys	Lys	Arg	Lys	Asn	Pro	Thr	Ser	Cys		
			820					825					830				
Ser	Arg	Arg	Phe	Tyr	Gln	Leu	Thr	Lys	Leu	Leu	Asp	Ser	Val	Gln	Pro		
		835					840					845					
Ile	Ala	Arg	Glu	Leu	His	Gln	Phe	Thr	Phe	Asp	Leu	Leu	Ile	Lys	Ser		
	850					855					860						
His	Met	Val	Ser	Val	Asp	Phe	Pro	Glu	Met	Met	Ala	Glu	Ile	Ile	Ser		
865					870					875					880		
Val	Gln	Val	Pro	Lys	Ile	Leu	Ser	Gly	Lys	Val	Lys	Pro	Ile	Tyr	Phe		
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His Thr Gln

<210> 21  
 <211> 2700  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

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```

<210> 22

<211> 4321

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 22

```

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```

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cggcggttc	gaagccgccg	cccggagctg	ccctttcctc	ttcgggtgaag	tttttaaaag	240
ctgctaaaga	ctcggaggaa	gcaaggaaaag	tgcttggtag	gactgacggc	tgctttgtc	300
ctcctcctct	ccaccccgcc	teccccacc	ctgccttccc	cccccccc	gtcttctctc	360
ccgcagctgc	ctcagtcggc	tactctcagc	caacccccct	caccaccctt	ctccccaccc	420
gcccccccg	ccccgtcggc	ccagcgctgc	cagccccgag	ttgcagagag	gtaactccct	480
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ctggggagcg	gcttcagcac	tgagccacgc	acccgcctgg	ttagaattcc	ggcggagaga	600
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agcagagatc	aaaagatgaa	aaggcagtc	ggtcttcagt	agccaaaaaa	caaaacaaac	720
aaaaacaaaa	aagccgaaat	aaaagaaaaa	gataataact	cagttcttat	ttgcacctac	780
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gtttagagag ctaagattat ctggggaaat caaaacaaaa aacaagcaaa caaaaaaaaaa 4320
a 4321

```

&lt;210&gt; 23

&lt;211&gt; 919

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 23

```

Met Glu Val Gln Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser
1           5           10           15
Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu
20           25           30
Val Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ala Ala
35           40           45
Pro Pro Gly Ala Ser Leu Leu Leu Leu Gln Gln Gln Gln Gln Gln Gln
50           55           60
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Glu Thr
65           70           75           80
Ser Pro Arg Gln Gln Gln Gln Gln Gln Gly Glu Asp Gly Ser Pro Gln
85           90           95
Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val Leu Asp Glu Glu Gln
100          105          110
Gln Pro Ser Gln Pro Gln Ser Ala Leu Glu Cys His Pro Glu Arg Gly
115          120          125
Cys Val Pro Glu Pro Gly Ala Ala Val Ala Ala Ser Lys Gly Leu Pro
130          135          140
Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp Ser Ala Ala Pro Ser
145          150          155          160
Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser Cys Ser
165          170          175
Ala Asp Leu Lys Asp Ile Leu Ser Glu Ala Ser Thr Met Gln Leu Leu
180          185          190
Gln Gln Gln Gln Gln Glu Ala Val Ser Glu Gly Ser Ser Ser Gly Arg
195          200          205
Ala Arg Glu Ala Ser Gly Ala Pro Thr Ser Ser Lys Asp Asn Tyr Leu
210          215          220
Gly Gly Thr Ser Thr Ile Ser Asp Asn Ala Lys Glu Leu Cys Lys Ala
225          230          235          240
Val Ser Val Ser Met Gly Leu Gly Val Glu Ala Leu Glu His Leu Ser
245          250          255
Pro Gly Glu Gln Leu Arg Gly Asp Cys Met Tyr Ala Pro Leu Leu Gly
260          265          270
Val Pro Pro Ala Val Arg Pro Thr Pro Cys Ala Pro Leu Ala Glu Cys
275          280          285
Lys Gly Ser Leu Leu Asp Asp Ser Ala Gly Lys Ser Thr Glu Asp Thr
290          295          300

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Ala	Glu	Tyr	Ser	Pro	Phe	Lys	Gly	Gly	Tyr	Thr	Lys	Gly	Leu	Glu	Gly	305	310	315	320
Glu	Ser	Leu	Gly	Cys	Ser	Gly	Ser	Ala	Ala	Ala	Gly	Ser	Ser	Gly	Thr	325	330	335	
Leu	Glu	Leu	Pro	Ser	Thr	Leu	Ser	Leu	Tyr	Lys	Ser	Gly	Ala	Leu	Asp	340	345	350	
Glu	Ala	Ala	Ala	Tyr	Gln	Ser	Arg	Asp	Tyr	Tyr	Asn	Phe	Pro	Leu	Ala	355	360	365	
Leu	Ala	Gly	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	His	Pro	His	Ala	Arg	370	375	380	
Ile	Lys	Leu	Glu	Asn	Pro	Leu	Asp	Tyr	Gly	Ser	Ala	Trp	Ala	Ala	Ala	385	390	395	400
Ala	Ala	Gln	Cys	Arg	Tyr	Gly	Asp	Leu	Ala	Ser	Leu	His	Gly	Ala	Gly	405	410	415	
Ala	Ala	Gly	Pro	Gly	Ser	Gly	Ser	Pro	Ser	Ala	Ala	Ala	Ser	Ser	Ser	420	425	430	
Trp	His	Thr	Leu	Phe	Thr	Ala	Glu	Glu	Gly	Gln	Leu	Tyr	Gly	Pro	Cys	435	440	445	
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	450	455	460	
Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Glu	Ala	Gly	Ala	Val	Ala	Pro	Tyr	465	470	475	480
Gly	Tyr	Thr	Arg	Pro	Pro	Gln	Gly	Leu	Ala	Gly	Gln	Glu	Ser	Asp	Phe	485	490	495	
Thr	Ala	Pro	Asp	Val	Trp	Tyr	Pro	Gly	Gly	Met	Val	Ser	Arg	Val	Pro	500	505	510	
Tyr	Pro	Ser	Pro	Thr	Cys	Val	Lys	Ser	Glu	Met	Gly	Pro	Trp	Met	Asp	515	520	525	
Ser	Tyr	Ser	Gly	Pro	Tyr	Gly	Asp	Met	Arg	Leu	Glu	Thr	Ala	Arg	Asp	530	535	540	
His	Val	Leu	Pro	Ile	Asp	Tyr	Tyr	Phe	Pro	Pro	Gln	Lys	Thr	Cys	Leu	545	550	555	560
Ile	Cys	Gly	Asp	Glu	Ala	Ser	Gly	Cys	His	Tyr	Gly	Ala	Leu	Thr	Cys	565	570	575	
Gly	Ser	Cys	Lys	Val	Phe	Phe	Lys	Arg	Ala	Ala	Glu	Gly	Lys	Gln	Lys	580	585	590	
Tyr	Leu	Cys	Ala	Ser	Arg	Asn	Asp	Cys	Thr	Ile	Asp	Lys	Phe	Arg	Arg	595	600	605	
Lys	Asn	Cys	Pro	Ser	Cys	Arg	Leu	Arg	Lys	Cys	Tyr	Glu	Ala	Gly	Met	610	615	620	
Thr	Leu	Gly	Ala	Arg	Lys	Leu	Lys	Lys	Leu	Gly	Asn	Leu	Lys	Leu	Gln	625	630	635	640
Glu	Glu	Gly	Glu	Ala	Ser	Ser	Thr	Thr	Ser	Pro	Thr	Glu	Glu	Thr	Thr	645	650	655	
Gln	Lys	Leu	Thr	Val	Ser	His	Ile	Glu	Gly	Tyr	Glu	Cys	Gln	Pro	Ile	660	665	670	
Phe	Leu	Asn	Val	Leu	Glu	Ala	Ile	Glu	Pro	Gly	Val	Val	Cys	Ala	Gly	675	680	685	
His	Asp	Asn	Asn	Gln	Pro	Asp	Ser	Phe	Ala	Ala	Leu	Leu	Ser	Ser	Leu	690	695	700	
Asn	Glu	Leu	Gly	Glu	Arg	Gln	Leu	Val	His	Val	Val	Lys	Trp	Ala	Lys	705	710	715	720
Ala	Leu	Pro	Gly	Phe	Arg	Asn	Leu	His	Val	Asp	Asp	Gln	Met	Ala	Val	725	730	735	
Ile	Gln	Tyr	Ser	Trp	Met	Gly	Leu	Met	Val	Phe	Ala	Met	Gly	Trp	Arg	740	745	750	
Ser	Phe	Thr	Asn	Val	Asn	Ser	Arg	Met	Leu	Tyr	Phe	Ala	Pro	Asp	Leu	755	760	765	
Val	Phe	Asn	Glu	Tyr	Arg	Met	His	Lys	Ser	Arg	Met	Tyr	Ser	Gln	Cys	770	775	780	

Val	Arg	Met	Arg	His	Leu	Ser	Gln	Glu	Phe	Gly	Trp	Leu	Gln	Ile	Thr	785	790	795	800
Pro	Gln	Glu	Phe	Leu	Cys	Met	Lys	Ala	Leu	Leu	Phe	Ser	Ile	Ile		805	810		815
Pro	Val	Asp	Gly	Leu	Lys	Asn	Gln	Lys	Phe	Phe	Asp	Glu	Leu	Arg	Met	820	825		830
Asn	Tyr	Ile	Lys	Glu	Leu	Asp	Arg	Ile	Ile	Ala	Cys	Lys	Arg	Lys	Asn	835	840		845
Pro	Thr	Ser	Cys	Ser	Arg	Arg	Phe	Tyr	Gln	Leu	Thr	Lys	Leu	Leu	Asp	850	855		860
Ser	Val	Gln	Pro	Ile	Ala	Arg	Glu	Leu	His	Gln	Phe	Thr	Phe	Asp	Leu	865	870		880
Leu	Ile	Lys	Ser	His	Met	Val	Ser	Val	Asp	Phe	Pro	Glu	Met	Met	Ala	885	890		895
Glu	Ile	Ile	Ser	Val	Gln	Val	Pro	Lys	Ile	Leu	Ser	Gly	Lys	Val	Lys	900	905		910
Pro	Ile	Tyr	Phe	His	Thr	Gln										915			

<210> 24

<211> 595

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 24

Met	Thr	Met	Thr	Leu	His	Thr	Lys	Ala	Ser	Gly	Met	Ala	Leu	Leu	His	1	5	10	15
Gln	Ile	Gln	Gly	Asn	Glu	Leu	Glu	Pro	Leu	Asn	Arg	Pro	Gln	Leu	Lys	20	25		30
Ile	Pro	Leu	Glu	Arg	Pro	Leu	Gly	Glu	Val	Tyr	Leu	Asp	Ser	Ser	Lys	35	40		45
Pro	Ala	Val	Tyr	Asn	Tyr	Pro	Glu	Gly	Ala	Ala	Tyr	Glu	Phe	Asn	Ala	50	55		60
Ala	Ala	Ala	Ala	Asn	Ala	Gln	Val	Tyr	Gly	Gln	Thr	Gly	Leu	Pro	Tyr	65	70		75
Gly	Pro	Gly	Ser	Glu	Ala	Ala	Ala	Phe	Gly	Ser	Asn	Gly	Leu	Gly	Gly	85	90		95
Phe	Pro	Pro	Leu	Asn	Ser	Val	Ser	Pro	Ser	Pro	Leu	Met	Leu	Leu	His	100	105		110
Pro	Pro	Pro	Gln	Leu	Ser	Pro	Phe	Leu	Gln	Pro	His	Gly	Gln	Gln	Val	115	120		125
Pro	Tyr	Tyr	Leu	Glu	Asn	Glu	Pro	Ser	Gly	Tyr	Thr	Val	Arg	Glu	Ala	130	135		140
Gly	Pro	Pro	Ala	Phe	Tyr	Arg	Pro	Asn	Ser	Asp	Asn	Arg	Arg	Gln	Gly	145	150		155
Gly	Arg	Glu	Arg	Leu	Ala	Ser	Thr	Asn	Asp	Lys	Gly	Ser	Met	Ala	Met	165	170		175
Glu	Ser	Ala	Lys	Glu	Thr	Arg	Tyr	Cys	Ala	Val	Cys	Asn	Asp	Tyr	Ala	180	185		190
Ser	Gly	Tyr	His	Tyr	Gly	Val	Trp	Ser	Cys	Glu	Gly	Cys	Lys	Ala	Phe	195	200		205
Phe	Lys	Arg	Ser	Ile	Gln	Gly	His	Asn	Asp	Tyr	Met	Cys	Pro	Ala	Thr	210	215		220
Asn	Gln	Cys	Thr	Ile	Asp	Lys	Asn	Arg	Arg	Lys	Ser	Cys	Gln	Ala	Cys	225	230		235
Arg	Leu	Arg	Lys	Cys	Tyr	Glu	Val	Gly	Met	Met	Lys	Gly	Gly	Ile	Arg	245	250		255



Lys Asp Arg Arg Gly Gly Arg Met Leu Lys His Lys Arg Gln Arg Asp  
260 265 270  
Asp Gly Glu Gly Arg Gly Glu Val Gly Ser Ala Gly Asp Met Arg Ala  
275 280 285  
Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys Asn  
290 295 300  
Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu Leu  
305 310 315 320  
Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg Pro  
325 330 335  
Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp Arg  
340 345 350  
Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe Val  
355 360 365  
Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp Leu  
370 375 380  
Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro Val  
385 390 395 400  
Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly Lys  
405 410 415  
Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ser  
420 425 430  
Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys Leu  
435 440 445  
Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser Ser  
450 455 460  
Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu Asp  
465 470 475 480  
Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu Thr  
485 490 495  
Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu Ser  
500 505 510  
His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met  
515 520 525  
Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu  
530 535 540  
Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser Val  
545 550 555 560  
Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser Ser  
565 570 575  
His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe Pro  
580 585 590  
Ala Thr Val  
595

<210> 25

<211> 6450

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 25

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gggagcccag	gagctggcgg	agggcgttcg	tcctggggagc	tgcaacttgct	ccgtcgggtc	180
gccggcttca	ccggaccgca	ggctcccggg	gcagggccgg	ggccagagct	cgcgtgtcgg	240
cgggacatgc	gctgcgtcgc	ctctaacctc	gggctgtgct	ctttttccag	gtggcccgcc	300
ggtttctgag	ccttctgccc	tgcggggaca	cggtctgcac	cctgcccgcg	gccacggacc	360

atgaccatga	ccctccacac	caaagcatct	gggatggccc	tactgcatca	gatccaaggg	420
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gaggtgtacc	tggacagcag	caagcccgcc	gtgtacaact	accccgaggg	cgccgcctac	540
gagttcaacg	ccgcggccgc	cgccaacgcg	caggtctacg	gtcagaccgg	cctccccctac	600
ggccccgggt	ctgaggctgc	ggcgttcggc	tccaacggcc	tgggggggtt	ccccccactc	660
aacagcgtgt	ctccgagccc	gctgatgcta	ctgcacccgc	cgccgcagct	gtcgcccttc	720
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<210> 26

<211> 614

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 26

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Leu Leu Arg Cys Ser Asp Ala Arg Arg Asp Leu Glu Leu Ala Ile Gly
      20             25             30
Gly Val Leu Arg Ala Glu Gln Gln Ile Lys Asp Asn Leu Arg Glu Val
      35             40             45

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Lys	Ala	Gln	Ile	His	Ser	Cys	Ile	Ser	Arg	His	Leu	Glu	Cys	Leu	Arg
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Ser	Arg	Glu	Val	Trp	Leu	Tyr	Glu	Gln	Val	Asp	Leu	Ile	Tyr	Gln	Leu
65					70					75					80
Lys	Glu	Glu	Thr	Leu	Gln	Gln	Gln	Ala	Gln	Gln	Leu	Tyr	Ser	Leu	Leu
				85					90					95	
Gly	Gln	Phe	Asn	Cys	Leu	Thr	His	Gln	Leu	Glu	Cys	Thr	Gln	Asn	Lys
			100					105					110		
Asp	Leu	Ala	Asn	Gln	Val	Ser	Val	Cys	Leu	Glu	Arg	Leu	Gly	Ser	Leu
		115					120					125			
Thr	Leu	Lys	Pro	Glu	Asp	Ser	Thr	Val	Leu	Leu	Phe	Glu	Ala	Asp	Thr
	130					135					140				
Ile	Thr	Leu	Arg	Gln	Thr	Ile	Thr	Thr	Phe	Gly	Ser	Leu	Lys	Thr	Ile
145					150					155					160
Gln	Ile	Pro	Glu	His	Leu	Met	Ala	His	Ala	Ser	Ser	Ala	Asn	Ile	Gly
				165					170					175	
Pro	Phe	Leu	Glu	Lys	Arg	Gly	Cys	Ile	Ser	Met	Pro	Glu	Gln	Lys	Ser
			180					185					190		
Ala	Ser	Gly	Ile	Val	Ala	Val	Pro	Phe	Ser	Glu	Trp	Leu	Leu	Gly	Ser
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Lys	Pro	Ala	Ser	Gly	Tyr	Gln	Ala	Pro	Tyr	Ile	Pro	Ser	Thr	Asp	Pro
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Gln	Asp	Trp	Leu	Thr	Gln	Lys	Gln	Thr	Leu	Glu	Asn	Ser	Gln	Thr	Ser
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Ser	Arg	Ala	Cys	Asn	Phe	Phe	Asn	Asn	Val	Gly	Gly	Asn	Leu	Lys	Gly
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Leu	Glu	Asn	Trp	Leu	Leu	Lys	Ser	Glu	Lys	Ser	Ser	Tyr	Gln	Lys	Cys
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Asn	Ser	His	Ser	Thr	Thr	Ser	Ser	Phe	Ser	Ile	Glu	Met	Glu	Lys	Val
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Gly	Asp	Gln	Glu	Leu	Pro	Asp	Gln	Asp	Glu	Met	Asp	Leu	Ser	Asp	Trp
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Leu	Val	Thr	Pro	Gln	Glu	Ser	His	Lys	Leu	Arg	Lys	Pro	Glu	Asn	Gly
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Ser	Arg	Glu	Thr	Ser	Glu	Lys	Phe	Lys	Leu	Leu	Phe	Gln	Ser	Tyr	Asn
				325					330					335	
Val	Asn	Asp	Trp	Leu	Val	Lys	Thr	Asp	Ser	Cys	Thr	Asn	Cys	Gln	Gly
			340					345					350		
Asn	Gln	Pro	Lys	Gly	Val	Glu	Ile	Glu	Asn	Leu	Gly	Asn	Leu	Lys	Cys
		355					360					365			
Leu	Asn	Asp	His	Leu	Glu	Ala	Lys	Lys	Pro	Leu	Ser	Thr	Pro	Ser	Met
	370					375					380				
Val	Thr	Glu	Asp	Trp	Leu	Val	Gln	Asn	His	Gln	Asp	Pro	Cys	Lys	Val
385					390					395					400
Glu	Glu	Val	Cys	Arg	Ala	Asn	Glu	Pro	Cys	Thr	Ser	Phe	Ala	Glu	Cys
				405					410					415	
Val	Cys	Asp	Glu	Asn	Cys	Glu	Lys	Glu	Ala	Leu	Tyr	Lys	Trp	Leu	Leu
			420					425					430		
Lys	Lys	Glu	Gly	Lys	Asp	Lys	Asn	Gly	Met	Pro	Val	Glu	Pro	Lys	Pro
		435					440					445			
Glu	Pro	Glu	Lys	His	Lys	Asp	Ser	Leu	Asn	Met	Trp	Leu	Cys	Pro	Arg
	450					455					460				
Lys	Glu	Val	Ile	Glu	Gln	Thr	Lys	Ala	Pro	Lys	Ala	Met	Thr	Pro	Ser
465					470					475					480
Arg	Ile	Ala	Asp	Ser	Phe	Gln	Val	Ile	Lys	Asn	Ser	Pro	Leu	Ser	Glu
				485					490					495	
Trp	Leu	Ile	Arg	Pro	Pro	Tyr	Lys	Glu	Gly	Ser	Pro	Lys	Glu	Val	Pro
			500					505					510		
Gly	Thr	Glu	Asp	Arg	Ala	Gly	Lys	Gln	Lys	Phe	Lys	Ser	Pro	Met	Asn
		515					520					525			

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Thr Ser Trp Cys Ser Phe Asn Thr Ala Asp Trp Val Leu Pro Gly Lys
530                    535                    540
Lys Met Gly Asn Leu Ser Gln Leu Ser Ser Gly Glu Asp Lys Trp Leu
545                    550                    555                    560
Leu Arg Lys Lys Ala Gln Glu Val Leu Leu Asn Ser Pro Leu Gln Glu
565                    570                    575
Glu His Asn Phe Pro Pro Asp His Tyr Gly Leu Pro Ala Val Cys Asp
580                    585                    590
Leu Phe Ala Cys Met Gln Leu Lys Val Asp Lys Glu Lys Trp Leu Tyr
595                    600                    605
Arg Thr Pro Leu Gln Met
610

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<210> 27  
 <211> 1845  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

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<400> 27
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attaaagata acttgcgaga ggtcaaagct cagattcaca gttgcataag ccgtcacctg      180
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<210> 28  
 <211> 474  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 28

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Gly	Gly	Glu	Thr	Arg	Ile	Tyr	Leu	Asp	Leu	Pro	Gln	Asn	Phe	Lys	Ile	35	40	45	
Phe	Val	Ser	Gly	Asn	Ser	Asn	Glu	Cys	Leu	Gln	Asn	Ser	Gly	Phe	Glu	50	55	60	
Tyr	Thr	Ile	Cys	Phe	Leu	Pro	Pro	Leu	Val	Leu	Asn	Phe	Glu	Leu	Pro	65	70	75	80
Pro	Asp	Tyr	Pro	Ser	Ser	Ser	Pro	Pro	Ser	Phe	Thr	Leu	Ser	Gly	Lys	85	90	95	
Trp	Leu	Ser	Pro	Thr	Gln	Leu	Ser	Ala	Leu	Cys	Lys	His	Leu	Asp	Asn	100	105	110	
Leu	Trp	Glu	Glu	His	Arg	Gly	Ser	Val	Val	Leu	Phe	Ala	Trp	Met	Gln	115	120	125	
Phe	Leu	Lys	Glu	Glu	Thr	Leu	Ala	Tyr	Leu	Asn	Ile	Val	Ser	Pro	Phe	130	135	140	
Glu	Leu	Lys	Ile	Gly	Ser	Gln	Lys	Lys	Val	Gln	Arg	Arg	Thr	Ala	Gln	145	150	155	160
Ala	Ser	Pro	Asn	Thr	Glu	Leu	Asp	Phe	Gly	Gly	Ala	Ala	Gly	Ser	Asp	165	170	175	
Val	Asp	Gln	Glu	Glu	Ile	Val	Asp	Glu	Arg	Ala	Val	Gln	Asp	Val	Glu	180	185	190	
Ser	Leu	Ser	Asn	Leu	Ile	Gln	Glu	Ile	Leu	Asp	Phe	Asp	Gln	Ala	Gln	195	200	205	
Gln	Ile	Lys	Cys	Phe	Asn	Ser	Lys	Leu	Phe	Leu	Cys	Ser	Ile	Cys	Phe	210	215	220	
Cys	Glu	Lys	Leu	Gly	Ser	Glu	Cys	Met	Tyr	Phe	Leu	Glu	Cys	Arg	His	225	230	235	240
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Val	Ala	Thr	Pro	Gly	Gln	Val	Lys	Glu	Leu	Val	Glu	Ala	Glu	Leu	Phe	275	280	285	
Ala	Arg	Tyr	Asp	Arg	Leu	Leu	Gln	Ser	Ser	Leu	Asp	Leu	Met	Ala		290	295	300	
Asp	Val	Val	Tyr	Cys	Pro	Arg	Pro	Cys	Cys	Gln	Leu	Pro	Val	Met	Gln	305	310	315	320
Glu	Pro	Gly	Cys	Thr	Met	Gly	Ile	Cys	Ser	Ser	Cys	Asn	Phe	Ala	Phe	325	330	335	
Cys	Thr	Leu	Cys	Arg	Leu	Thr	Tyr	His	Gly	Val	Ser	Pro	Cys	Lys	Val	340	345	350	
Thr	Ala	Glu	Lys	Leu	Met	Asp	Leu	Arg	Asn	Glu	Tyr	Leu	Gln	Ala	Asp	355	360	365	
Glu	Ala	Asn	Lys	Arg	Leu	Leu	Asp	Gln	Arg	Tyr	Gly	Lys	Arg	Val	Ile	370	375	380	
Gln	Lys	Ala	Leu	Glu	Glu	Met	Glu	Ser	Lys	Glu	Trp	Leu	Glu	Lys	Asn	385	390	395	400
Ser	Lys	Ser	Cys	Pro	Cys	Cys	Gly	Thr	Pro	Ile	Glu	Lys	Leu	Asp	Gly	405	410	415	
Cys	Asn	Lys	Met	Thr	Cys	Thr	Gly	Cys	Met	Gln	Tyr	Phe	Cys	Trp	Ile	420	425	430	
Cys	Met	Gly	Ser	Leu	Ser	Arg	Ala	Asn	Pro	Tyr	Lys	His	Phe	Asn	Asp	435	440	445	

Pro Gly Ser Pro Cys Phe Asn Arg Leu Phe Tyr Ala Val Asp Val Asp  
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 Asp Asp Ile Trp Glu Asp Glu Val Glu Asp  
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<210> 29  
 <211> 1701  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

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 gcagagtctg tccaagggtgg agaaaccagg atctattttgg atttgccaca gaatttcaag 180  
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 cagcagataa aatgctttaa tagtaaattg ttctgtgca gtatctgttt ctgtgagaag 720  
 ctgggtagtg aatgcatgta cttcttggag tgcaggcatg tgtactgcaa agcctgtctg 780  
 aaggactact ttgaaatcca gatcagagat ggccagggttc aatgcctcaa ctgcccagaa 840  
 ccaaagtgcc cttcgggtggc cactcctggg cagggtcaaag agttagtga agcagagtta 900  
 tttgcccgtt atgaccgcct tctcctccag tctccttgg accctgatggc agatgtggtg 960  
 tactgcccc ggccgtgctg ccagctgcct gtgatgcagg aacctggctg caccatgggt 1020  
 atctgctcca gctgcaattt tgccttctgt actttgtgca ggttgacctt ccatggggtc 1080  
 tccccatgta aggtgactgc agagaaatta atggacttac gaaatgaata cctgcaagcg 1140  
 gatgaggcta ataaaagact tttggatcaa aggtatggta agagagtgat tcagaaggca 1200  
 ctggaagaga tggaaagtaa ggagtggcta gagaagaact caaagagctg cccatgttgt 1260  
 ggaactccca tagagaaatt agacggatgt aacaagatga catgtactgg ctgtatgcaa 1320  
 tattttctgtt ggatttgcct gggttctctc tctagagcaa acccttatac acatttcaat 1380  
 gaccctgggt caccatgttt taaccggctg ttttatgctg tggatgttga cgacgatatt 1440  
 tgggaagatg aggtagaaga ctagttaact actgtcaaag atatggaagt ggattgtttt 1500  
 tccctaatact tccgtcaagt acacaaagta actttgcggg atattttagg tactattcat 1560  
 tcaactcttc tgcgtagaag atatggaaga acgaggttta tattttcatg tggatctact 1620  
 gaagaagggt cattgatata tttttaaatg taagttgaga aaaatttata agccaaagggt 1680  
 tcagaaaatt aaactacaga a 1701

<210> 30  
 <211> 444  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 30  
 Met Pro Arg Ser Gly Ala Pro Lys Glu Arg Pro Ala Glu Pro Leu Thr  
 1 5 10 15  
 Pro Pro Pro Ser Tyr Gly His Gln Pro Gln Thr Gly Ser Gly Glu Ser  
 20 25 30

Ser	Gly	Ala	Ser	Gly	Asp	Lys	Asp	His	Leu	Tyr	Ser	Thr	Val	Cys	Lys
	35						40					45			
Pro	Arg	Ser	Pro	Lys	Pro	Ala	Ala	Pro	Ala	Ala	Pro	Pro	Phe	Ser	Ser
	50					55					60				
Ser	Ser	Gly	Val	Leu	Gly	Thr	Gly	Leu	Cys	Glu	Leu	Asp	Arg	Leu	Leu
65					70					75					80
Gln	Glu	Leu	Asn	Ala	Thr	Gln	Phe	Asn	Ile	Thr	Asp	Glu	Ile	Met	Ser
			85						90					95	
Gln	Phe	Pro	Ser	Ser	Lys	Val	Ala	Ser	Gly	Glu	Gln	Lys	Glu	Asp	Gln
			100					105					110		
Ser	Glu	Asp	Lys	Lys	Arg	Pro	Ser	Leu	Pro	Ser	Ser	Pro	Ser	Pro	Gly
	115						120					125			
Leu	Pro	Lys	Ala	Ser	Ala	Thr	Ser	Ala	Thr	Leu	Glu	Leu	Asp	Arg	Leu
	130					135					140				
Met	Ala	Ser	Leu	Pro	Asp	Phe	Arg	Val	Gln	Asn	His	Leu	Pro	Ala	Ser
145					150					155					160
Gly	Pro	Thr	Gln	Pro	Pro	Val	Val	Ser	Ser	Thr	Asn	Glu	Gly	Ser	Pro
			165						170					175	
Ser	Pro	Pro	Glu	Pro	Thr	Ala	Lys	Gly	Ser	Leu	Asp	Thr	Met	Leu	Gly
			180					185					190		
Leu	Leu	Gln	Ser	Asp	Leu	Ser	Arg	Arg	Gly	Val	Pro	Thr	Gln	Ala	Lys
	195						200					205			
Gly	Leu	Cys	Gly	Ser	Cys	Asn	Lys	Pro	Ile	Ala	Gly	Gln	Val	Val	Thr
	210					215					220				
Ala	Leu	Gly	Arg	Ala	Trp	His	Pro	Glu	His	Phe	Val	Cys	Gly	Gly	Cys
225					230					235					240
Ser	Thr	Ala	Leu	Gly	Gly	Ser	Ser	Phe	Phe	Glu	Lys	Asp	Gly	Ala	Pro
			245						250					255	
Phe	Cys	Pro	Glu	Cys	Tyr	Phe	Glu	Arg	Phe	Ser	Pro	Arg	Cys	Gly	Phe
			260					265					270		
Cys	Asn	Gln	Pro	Ile	Arg	His	Lys	Met	Val	Thr	Ala	Leu	Gly	Thr	His
	275						280					285			
Trp	His	Pro	Glu	His	Phe	Cys	Cys	Val	Ser	Cys	Gly	Glu	Pro	Phe	Gly
	290					295					300				
Asp	Glu	Gly	Phe	His	Glu	Arg	Glu	Gly	Arg	Pro	Tyr	Cys	Arg	Arg	Asp
305					310					315					320
Phe	Leu	Gln	Leu	Phe	Ala	Pro	Arg	Cys	Gln	Gly	Cys	Gln	Gly	Pro	Ile
			325						330					335	
Leu	Asp	Asn	Tyr	Ile	Ser	Ala	Leu	Ser	Leu	Leu	Trp	His	Pro	Asp	Cys
			340					345					350		
Phe	Val	Cys	Arg	Glu	Cys	Phe	Ala	Pro	Phe	Ser	Gly	Gly	Ser	Phe	Phe
		355					360					365			
Glu	His	Glu	Gly	Arg	Pro	Leu	Cys	Glu	Asn	His	Phe	His	Ala	Arg	Arg
	370					375					380				
Gly	Ser	Leu	Trp	Pro	Thr	Cys	Gly	Leu	Pro	Val	Thr	Gly	Arg	Cys	Val
385					390					395					400
Ser	Ala	Leu	Gly	Arg	Arg	Phe	His	Pro	Asp	His	Phe	Ala	Cys	Thr	Phe
			405						410					415	
Cys	Leu	Arg	Pro	Leu	Thr	Lys	Gly	Ser	Phe	Gln	Glu	Arg	Ala	Gly	Lys
			420					425					430		
Pro	Tyr	Cys	Gln	Pro	Cys	Phe	Leu	Lys	Leu	Phe	Gly				
	435						440								

<210> 31

<211> 1335

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct



&lt;400&gt; 31

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atgccaaagggt cagggggctcc caaagagcgc cctgcgggagc ctctcaccctc tcccccatcc      60

tatggccacc agccacagac aggggtctggg gagtcttcag gagcctcggg ggacaaggac      120
cacctgtaca gcacgggatg caagcctcgg tccccaaagc ctgcagcccc ggccgcccct      180
ccattctcct cttccagcgg tgtcttgggt accgggctct gtgagctaga tcggttgctt      240
caggaactta atgccactca gttcaacatc acagatgaaa tcatgtctca gttcccatct      300
agcaagggtg cttcaggaga gcagaaggag gaccagtctg aagataagaa aagaccagc      360
ctcccttcca gcccgtctcc tggcctccca aaggcttctg ccacctcagc cactctggag      420
ctggatagac tgatggcctc actccctgac ttccgcgttc aaaaccatct tccagcctct      480
gggccaactc agccaccggt ggtgagctcc acaaatgagg gctccccatc cccaccagag      540
ccgactgcaa agggcagcct agacaccatg ctggggctgc tgcagtccga cctcagccgc      600
cgggggtgttc ccaccaggc caaaggcctc tgtggctcct gcaataaacc tattgctggg      660
caagtgggtga cggctctggg ccgcgcctgg ccccccgagc acttcgtttg cggaggctgt      720
tccaccgccc tgggaggcag cagcttcttc gagaaggatg gagccccctt ctgccccgag      780
tgctactttg agcgttctc gccaaagatgt ggcttctgca accagcccat ccgacacaag      840
atggtgaccg ccttgggcac tcaactggcag ccagagcatt tctgctgcgt cagttgcggg      900
gagcccttcg gagatgaggg tttccacgag cgcgagggcc gcccctactg ccgcccgggac      960
ttcctgcagc tgttcgcccc gcgctgccag ggctgccagg gcccctactc ggataactac     1020
atctcggcgc tcagcctgct ctggcaccgc gactgtttcg tctgcaggga atgcttcgcg     1080
cccttctcgg gaggcagctt ttctcagcac gagggccgcg cgttgtgcga gaaccacttc     1140
cacgcacgac gcggctcgct gtggcccacg tgtggcctcc ctgtgaccgg ccgctgcgtg     1200
tcggccctgg gtcgccgctt ccaccgggac cacttcgcat gcaccttctg cctgcgcccg     1260
ctcaccaagg ggtccttcca ggagcgcgcc ggcaagccct actgccagcc ctgcttctcg     1320
aagctcttcg gctga                                     1335

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&lt;210&gt; 32

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 32

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Met Ala Ala Gln Gly Glu Pro Gln Val Gln Phe Lys Leu Val Leu Val
1           5           10           15
Gly Asp Gly Gly Thr Gly Lys Thr Thr Phe Val Lys Arg His Leu Thr
20          25          30
Gly Glu Phe Glu Lys Lys Tyr Val Ala Thr Leu Gly Val Glu Val His
35          40          45
Pro Leu Val Phe His Thr Asn Arg Gly Pro Ile Lys Phe Asn Val Trp
50          55          60
Asp Thr Ala Gly Gln Glu Lys Phe Gly Gly Leu Arg Asp Gly Tyr Tyr
65          70          75          80
Ile Gln Ala Gln Cys Ala Ile Ile Met Phe Asp Val Thr Ser Arg Val
85          90          95
Thr Tyr Lys Asn Val Pro Asn Trp His Arg Asp Leu Val Arg Val Cys
100         105         110
Glu Asn Ile Pro Ile Val Leu Cys Gly Asn Lys Val Asp Ile Lys Asp
115         120         125
Arg Lys Val Lys Ala Lys Ser Ile Val Phe His Arg Lys Lys Asn Leu
130         135         140
Gln Tyr Tyr Asp Ile Ser Ala Lys Ser Asn Tyr Asn Phe Glu Lys Pro
145         150         155         160
Phe Leu Trp Leu Ala Arg Lys Leu Ile Gly Asp Pro Asn Leu Glu Phe
165         170         175
Val Ala Met Pro Ala Leu Ala Pro Pro Glu Val Val Met Asp Pro Ala
180         185         190

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Leu Ala Ala Gln Tyr Glu His Asp Leu Glu Val Ala Gln Thr Thr Ala  
 195 200 205  
 Leu Pro Asp Glu Asp Asp Asp Leu  
 210 215

<210> 33  
 <211> 1566  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 33  
 ggcgcttctg gaaggaacgc cgcgatggct gcgcagggag agccccaggt ccagttcaaa 60  
 cttgtattgg ttggtgatgg tggtagtgga aaaacgacct tcgtgaaacg tcatttgact 120  
 ggtgaatttg agaagaagta tgtagccacc ttgggtggtg aggttcaccc cctagtgttc 180  
 cacaccaaca gaggacctat taagttcaat gtatgggaca cagccggcca ggagaaattc 240  
 ggtggactga gagatggcta ttatatccaa gccagtggtg ccatcataat gtttgatgta 300  
 acatcgagag ttacttacaa gaatgtgcct aactggcata gagatctggt acgagtgtgt 360  
 gaaaacatcc ccattgtggt gtgtggcaac aaagtggata ttaaggacag gaaagtgaag 420  
 gcgaaatcca ttgtcttcca ccgaaagaag aatcttcagt actacgacat ttctgccaaa 480  
 agtaactaca actttgaaaa gcccttcctc tggcttgcta ggaagctcat tggagaccct 540  
 aacttggaat ttgttgccat gcctgctctc gccccaccag aagttgtcat ggaccagct 600  
 ttggcagcac agtatgagca cgacttagag gttgctcaga caactgctct cccggatgag 660  
 gatgatgacc tgtgagaatg aagctggagc ccagcgtcag aagtctagtt ttataggcag 720  
 ctgtcctgtg atgtcagcgg tgcagcgtgt gtgccacctc attattatct agctaagcgg 780  
 aacatgtgct ttatctgtgg gatgctgaag gagatgagtg ggcttcggag tgaatgtggc 840  
 agtttaaaaa ataacttcat tgtttggacc tgcataattta gctgtttgga cgcagttgat 900  
 tccttgagtt tcataataa gactgctgca gtcacatcac aatattcagt ggtgaaatct 960  
 tgtttgttac tgtcattccc attccttttc tttagaatca gaataaagtt gtatttcaaa 1020  
 tatctaagca agtgaactca tcccttggtt ataaatagca tttggaaacc actaaagtag 1080  
 ggaagtttta tgccatgtta atatttgaat tgccttgctt ttatcactta atttgaaatc 1140  
 tattgggtta atttctccct atgtttatgt ttgtacattt gagccatgtc acacaaactg 1200  
 atgatgacag gtcagcagta ttctatttgg ttagaagggt tacatgggtg aaatattagt 1260  
 gcagttaagc taaagcagtg tttgctccac cttcatattg gctaggtagg gtcacctagg 1320  
 gaagcacttg ctcaaaatct gtgacctgtc agaataaaaa tgtggtttgt acatatcaaa 1380  
 tagatatttt aagggttaata ttttctttta tggcaaaagt aatcatgttt taatgtagaa 1440  
 cctcaaacag gatggaacat cagtggatgg caggagggtg ggaattcttg ctgttaaaaa 1500  
 taattacaaa ttttgcaatt tttgtttgaa tgtagatgac ttagtgtgaa gttgatacgc 1560  
 aagccg 1566

<210> 34  
 <211> 2427  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 34  
 Met Pro Leu Lys Thr Arg Thr Ala Leu Ser Asp Asp Pro Asp Ser Ser  
 1 5 10 15  
 Thr Ser Thr Leu Gly Asn Met Leu Glu Leu Pro Gly Thr Ser Ser Ser  
 20 25 30  
 Ser Thr Ser Gln Glu Leu Pro Phe Cys Gln Pro Lys Lys Lys Ser Thr  
 35 40 45  
 Pro Leu Lys Tyr Glu Val Gly Asp Leu Ile Trp Ala Lys Phe Lys Arg  
 50 55 60

Arg	Pro	Trp	Trp	Pro	Cys	Arg	Ile	Cys	Ser	Asp	Pro	Leu	Ile	Asn	Thr
65					70					75					80
His	Ser	Lys	Met	Lys	Val	Ser	Asn	Arg	Arg	Pro	Tyr	Arg	Gln	Tyr	Tyr
				85					90					95	
Val	Glu	Ala	Phe	Gly	Asp	Pro	Ser	Glu	Arg	Ala	Trp	Val	Ala	Gly	Lys
			100					105					110		
Ala	Ile	Val	Met	Phe	Glu	Gly	Arg	His	Gln	Phe	Glu	Glu	Leu	Pro	Val
		115					120					125			
Leu	Arg	Arg	Arg	Gly	Lys	Gln	Lys	Glu	Lys	Gly	Tyr	Arg	His	Lys	Val
	130					135					140				
Pro	Gln	Lys	Ile	Leu	Ser	Lys	Trp	Glu	Ala	Ser	Val	Gly	Leu	Ala	Glu
145					150					155					160
Gln	Tyr	Asp	Val	Pro	Lys	Gly	Ser	Lys	Asn	Arg	Lys	Cys	Ile	Pro	Gly
				165					170					175	
Ser	Ile	Lys	Leu	Asp	Ser	Glu	Glu	Asp	Met	Pro	Phe	Glu	Asp	Cys	Thr
			180					185					190		
Asn	Asp	Pro	Glu	Ser	Glu	His	Asp	Leu	Leu	Leu	Asn	Gly	Cys	Leu	Lys
	195						200					205			
Ser	Leu	Ala	Phe	Asp	Ser	Glu	His	Ser	Ala	Asp	Glu	Lys	Glu	Lys	Pro
	210					215					220				
Cys	Ala	Lys	Ser	Arg	Ala	Arg	Lys	Ser	Ser	Asp	Asn	Pro	Lys	Arg	Thr
225					230					235					240
Ser	Val	Lys	Lys	Gly	His	Ile	Gln	Phe	Glu	Ala	His	Lys	Asp	Glu	Arg
				245					250					255	
Arg	Gly	Lys	Ile	Pro	Glu	Asn	Leu	Gly	Leu	Asn	Phe	Ile	Ser	Gly	Asp
			260					265					270		
Ile	Ser	Asp	Thr	Gln	Ala	Ser	Asn	Glu	Leu	Ser	Arg	Ile	Ala	Asn	Ser
			275					280				285			
Leu	Thr	Gly	Ser	Asn	Thr	Ala	Pro	Gly	Ser	Phe	Leu	Phe	Ser	Ser	Cys
	290					295					300				
Gly	Lys	Asn	Thr	Ala	Lys	Lys	Glu	Phe	Glu	Thr	Ser	Asn	Gly	Asp	Ser
305					310					315					320
Leu	Leu	Gly	Leu	Pro	Glu	Gly	Ala	Leu	Ile	Ser	Lys	Cys	Ser	Arg	Glu
				325				330					335		
Lys	Asn	Lys	Pro	Gln	Arg	Ser	Leu	Val	Cys	Gly	Ser	Lys	Val	Lys	Leu
			340					345					350		
Cys	Tyr	Ile	Gly	Ala	Gly	Asp	Glu	Glu	Lys	Arg	Ser	Asp	Ser	Ile	Ser
	355					360						365			
Ile	Cys	Thr	Thr	Ser	Asp	Asp	Gly	Ser	Ser	Asp	Leu	Asp	Pro	Ile	Glu
	370					375					380				
His	Ser	Ser	Glu	Ser	Asp	Asn	Ser	Val	Leu	Glu	Ile	Pro	Asp	Ala	Phe
385					390					395					400
Asp	Arg	Thr	Glu	Asn	Met	Leu	Ser	Met	Gln	Lys	Asn	Glu	Lys	Ile	Lys
				405					410					415	
Tyr	Ser	Arg	Phe	Ala	Ala	Thr	Asn	Thr	Arg	Val	Lys	Ala	Lys	Gln	Lys
			420					425					430		
Pro	Leu	Ile	Ser	Asn	Ser	His	Thr	Asp	His	Leu	Met	Gly	Cys	Thr	Lys
	435					440						445			
Ser	Ala	Glu	Pro	Gly	Thr	Glu	Thr	Ser	Gln	Val	Asn	Leu	Ser	Asp	Leu
	450					455					460				
Lys	Ala	Ser	Thr	Leu	Val	His	Lys	Pro	Gln	Ser	Asp	Phe	Thr	Asn	Asp
465					470					475					480
Ala	Leu	Ser	Pro	Lys	Phe	Asn	Leu	Ser	Ser	Ser	Ile	Ser	Ser	Glu	Asn
				485					490					495	
Ser	Leu	Ile	Lys	Gly	Gly	Ala	Ala	Asn	Gln	Ala	Leu	Leu	His	Ser	Lys
			500					505					510		
Ser	Lys	Gln	Pro	Lys	Phe	Arg	Ser	Ile	Lys	Cys	Lys	His	Lys	Glu	Asn
	515						520					525			
Pro	Val	Met	Ala	Glu	Pro	Pro	Val	Ile	Asn	Glu	Glu	Cys	Ser	Leu	Lys
	530					535					540				

Cys	Cys	Ser	Ser	Asp	Thr	Lys	Gly	Ser	Pro	Leu	Ala	Ser	Ile	Ser	Lys
545					550					555					560
Ser	Gly	Lys	Val	Asp	Gly	Leu	Lys	Leu	Leu	Asn	Asn	Met	His	Glu	Lys
				565					570					575	
Thr	Arg	Asp	Ser	Ser	Asp	Ile	Glu	Thr	Ala	Val	Val	Lys	His	Val	Leu
			580					585					590		
Ser	Glu	Leu	Lys	Glu	Leu	Ser	Tyr	Arg	Ser	Leu	Gly	Glu	Asp	Val	Ser
		595					600					605			
Asp	Ser	Gly	Thr	Ser	Lys	Pro	Ser	Lys	Pro	Leu	Leu	Phe	Ser	Ser	Ala
	610					615					620				
Ser	Ser	Gln	Asn	His	Ile	Pro	Ile	Glu	Pro	Asp	Tyr	Lys	Phe	Ser	Thr
625					630					635					640
Leu	Leu	Met	Met	Leu	Lys	Asp	Met	His	Asp	Ser	Lys	Thr	Lys	Glu	Gln
				645					650					655	
Arg	Leu	Met	Thr	Ala	Gln	Asn	Leu	Val	Ser	Tyr	Arg	Ser	Pro	Gly	Arg
			660					665					670		
Gly	Asp	Cys	Ser	Thr	Asn	Ser	Pro	Val	Gly	Val	Ser	Lys	Val	Leu	Val
	675						680					685			
Ser	Gly	Gly	Ser	Thr	His	Asn	Ser	Glu	Lys	Lys	Gly	Asp	Gly	Thr	Gln
	690					695					700				
Asn	Ser	Ala	Asn	Pro	Ser	Pro	Ser	Gly	Gly	Asp	Ser	Ala	Leu	Ser	Gly
705					710					715					720
Glu	Leu	Ser	Ala	Ser	Leu	Pro	Gly	Leu	Leu	Ser	Asp	Lys	Arg	Asp	Leu
				725					730					735	
Pro	Ala	Ser	Gly	Lys	Ser	Arg	Ser	Asp	Cys	Val	Thr	Arg	Arg	Asn	Cys
			740				745						750		
Gly	Arg	Ser	Lys	Pro	Ser	Ser	Lys	Leu	Arg	Asp	Ala	Phe	Ser	Ala	Gln
	755						760					765			
Met	Val	Lys	Asn	Thr	Val	Asn	Arg	Lys	Ala	Leu	Lys	Thr	Glu	Arg	Lys
	770					775					780				
Arg	Lys	Leu	Asn	Gln	Leu	Pro	Ser	Val	Thr	Leu	Asp	Ala	Val	Leu	Gln
785					790					795					800
Gly	Asp	Arg	Glu	Arg	Gly	Gly	Ser	Leu	Arg	Gly	Gly	Ala	Glu	Asp	Pro
			805						810					815	
Ser	Lys	Glu	Asp	Pro	Leu	Gln	Ile	Met	Gly	His	Leu	Thr	Ser	Glu	Asp
			820					825					830		
Gly	Asp	His	Phe	Ser	Asp	Val	His	Phe	Asp	Ser	Lys	Val	Lys	Gln	Ser
	835						840					845			
Asp	Pro	Gly	Lys	Ile	Ser	Glu	Lys	Gly	Leu	Ser	Phe	Glu	Asn	Gly	Lys
	850					855					860				
Gly	Pro	Glu	Leu	Asp	Ser	Val	Met	Asn	Ser	Glu	Asn	Asp	Glu	Leu	Asn
865					870					875					880
Gly	Val	Asn	Gln	Val	Val	Pro	Lys	Lys	Arg	Trp	Gln	Arg	Leu	Asn	Gln
			885						890					895	
Arg	Arg	Thr	Lys	Pro	Arg	Lys	Arg	Met	Asn	Arg	Phe	Lys	Glu	Lys	Glu
			900					905					910		
Asn	Ser	Glu	Cys	Ala	Phe	Arg	Val	Leu	Leu	Pro	Ser	Asp	Pro	Val	Gln
	915						920					925			
Glu	Gly	Arg	Asp	Glu	Phe	Pro	Glu	His	Arg	Thr	Pro	Ser	Ala	Ser	Ile
	930					935					940				
Leu	Glu	Glu	Pro	Leu	Thr	Glu	Gln	Asn	His	Ala	Asp	Cys	Leu	Asp	Ser
945					950					955					960
Ala	Gly	Pro	Arg	Leu	Asn	Val	Cys	Asp	Lys	Ser	Ser	Ala	Ser	Ile	Gly
				965					970					975	
Asp	Met	Glu	Lys	Glu	Pro	Gly	Ile	Pro	Ser	Leu	Thr	Pro	Gln	Ala	Glu
			980					985					990		
Leu	Pro	Glu	Pro	Ala	Val	Arg	Ser	Glu	Lys	Lys	Arg	Leu	Arg	Lys	Pro
		995					1000					1005			
Ser	Lys	Trp	Leu	Leu	Glu	Tyr	Thr	Glu	Glu	Tyr	Asp	Gln	Ile	Phe	Ala
	1010					1015					1020				



Ile Cys His Pro Arg	Ala Val Pro Ser Asn	Ile Asp Lys Met Arg His	1505	1510	1515	1520
Asp Val Gly Glu Phe	Pro Val Leu Phe Phe Gly Ser Asn Asp Tyr Leu		1525	1530	1535	
Trp Thr His Gln Ala Arg Val Phe	Pro Tyr Met Glu Gly Asp Val Ser		1540	1545	1550	
Ser Lys Asp Lys Met Gly Lys Gly Val Asp Gly Thr Tyr Lys Lys Ala			1555	1560	1565	
Leu Gln Glu Ala Ala Ala Arg Phe Glu Glu Leu Lys Ala Gln Lys Glu			1570	1575	1580	
Leu Arg Gln Leu Gln Glu Asp Arg Lys Asn Asp Lys Lys Pro Pro Pro			1585	1590	1595	1600
Tyr Lys His Ile Lys Val Asn Arg Pro Ile Gly Arg Val Gln Ile Phe			1605	1610	1615	
Thr Ala Asp Leu Ser Glu Ile Pro Arg Cys Asn Cys Lys Ala Thr Asp			1620	1625	1630	
Glu Asn Pro Cys Gly Ile Asp Ser Glu Cys Ile Asn Arg Met Leu Leu			1635	1640	1645	
Tyr Glu Cys His Pro Thr Val Cys Pro Ala Gly Gly Arg Cys Gln Asn			1650	1655	1660	
Gln Cys Phe Ser Lys Arg Gln Tyr Pro Glu Val Glu Ile Phe Arg Thr			1665	1670	1675	1680
Leu Gln Arg Gly Trp Gly Leu Arg Thr Lys Thr Asp Ile Lys Lys Gly			1685	1690	1695	
Glu Phe Val Asn Glu Tyr Val Gly Glu Leu Ile Asp Glu Glu Glu Cys			1700	1705	1710	
Arg Ala Arg Ile Arg Tyr Ala Gln Glu His Asp Ile Thr Asn Phe Tyr			1715	1720	1725	
Met Leu Thr Leu Asp Lys Asp Arg Ile Ile Asp Ala Gly Pro Lys Gly			1730	1735	1740	
Asn Tyr Ala Arg Phe Met Asn His Cys Cys Gln Pro Asn Cys Glu Thr			1745	1750	1755	1760
Gln Lys Trp Ser Val Asn Gly Asp Thr Arg Val Gly Leu Phe Ala Leu			1765	1770	1775	
Ser Asp Ile Lys Ala Gly Thr Glu Leu Thr Phe Asn Tyr Asn Leu Glu			1780	1785	1790	
Cys Leu Gly Asn Gly Lys Thr Val Cys Lys Cys Gly Ala Pro Asn Cys			1795	1800	1805	
Ser Gly Phe Leu Gly Val Arg Pro Lys Asn Gln Pro Ile Ala Thr Glu			1810	1815	1820	
Glu Lys Ser Lys Lys Phe Lys Lys Lys Gln Gln Gly Lys Arg Arg Thr			1825	1830	1835	1840
Gln Gly Glu Ile Thr Lys Glu Arg Glu Asp Glu Cys Phe Ser Cys Gly			1845	1850	1855	
Asp Ala Gly Gln Leu Val Ser Cys Lys Lys Pro Gly Cys Pro Lys Val			1860	1865	1870	
Tyr His Ala Asp Cys Leu Asn Leu Thr Lys Arg Pro Ala Gly Lys Trp			1875	1880	1885	
Glu Cys Pro Trp His Gln Cys Asp Ile Cys Gly Lys Glu Ala Ala Ser			1890	1895	1900	
Phe Cys Glu Met Cys Pro Ser Ser Phe Cys Lys Gln His Arg Glu Gly			1905	1910	1915	1920
Met Leu Phe Ile Ser Lys Leu Asp Gly Arg Leu Ser Cys Thr Glu His			1925	1930	1935	
Asp Pro Cys Gly Pro Asn Pro Leu Glu Pro Gly Glu Ile Arg Glu Tyr			1940	1945	1950	
Val Pro Pro Pro Val Pro Leu Pro Pro Gly Pro Ser Thr His Leu Ala			1955	1960	1965	
Glu Gln Ser Thr Gly Met Ala Ala Gln Ala Pro Lys Met Ser Asp Lys			1970	1975	1980	

Pro	Pro	Ala	Asp	Thr	Asn	Gln	Met	Leu	Ser	Leu	Ser	Lys	Lys	Ala	Leu	1985	1990	1995	2000
Ala	Gly	Thr	Cys	Gln	Arg	Pro	Leu	Leu	Pro	Glu	Arg	Pro	Leu	Glu	Arg	2005	2010	2015	
Thr	Asp	Ser	Arg	Pro	Gln	Pro	Leu	Asp	Lys	Val	Arg	Asp	Leu	Ala	Gly	2020	2025	2030	
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Leu	Glu	Arg	Pro	Leu	Gly	Thr	Ala	Asp	Pro	Arg	Leu	Asp	Lys	Ser	Ile	2085	2090	2095	
Gly	Ala	Ala	Ser	Pro	Arg	Pro	Gln	Ser	Leu	Glu	Lys	Thr	Ser	Val	Pro	2100	2105	2110	
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Pro	Lys	Pro	Gln	Thr	Ser	Asp	Arg	Pro	Thr	Asp	Lys	Pro	His	Ala	Ser	2130	2135	2140	
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Gln	Thr	Leu	Val	Ala	Lys	Glu	Lys	Ala	Leu	Arg	Pro	Val	Asp	Gln	Asn	2165	2170	2175	
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Thr	Pro	Arg	Gln	Lys	Glu	Arg	Ala	Ala	Ser	Pro	His	Gln	Val	Thr	Pro	2195	2200	2205	
Gln	Ala	Asp	Glu	Lys	Met	Pro	Val	Leu	Glu	Ser	Ser	Ser	Trp	Pro	Ala	2210	2215	2220	
Ser	Lys	Gly	Leu	Gly	His	Met	Pro	Arg	Ala	Val	Glu	Lys	Gly	Cys	Val	2225	2230	2235	2240
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Pro	Pro	Ala	Lys	Ala	Phe	Leu	Tyr	Glu	Pro	Thr	Thr	Gln	Ala	Ser	Gly	2275	2280	2285	
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Pro	Ala	Leu	Ala	Ala	Lys	Ser	Gly	Gln	Ser	Phe	Arg	Ser	Leu	Gly	Lys	2325	2330	2335	
Ala	Pro	Ala	Ser	Leu	Pro	Thr	Glu	Glu	Lys	Lys	Leu	Val	Thr	Thr	Glu	2340	2345	2350	
Gln	Ser	Pro	Trp	Ala	Leu	Gly	Lys	Ala	Ser	Ser	Arg	Ala	Gly	Leu	Trp	2355	2360	2365	
Pro	Ile	Val	Ala	Gly	Gln	Thr	Leu	Ala	Gln	Ser	Cys	Trp	Ser	Ala	Gly	2370	2375	2380	
Ser	Thr	Gln	Thr	Leu	Ala	Gln	Thr	Cys	Trp	Ser	Leu	Gly	Arg	Gly	Gln	2385	2390	2395	2400
Asp	Pro	Lys	Pro	Glu	Gln	Asn	Thr	Leu	Pro	Ala	Leu	Asn	Gln	Ala	Pro	2405	2410	2415	
Ser	Ser	His	Lys	Cys	Ala	Glu	Ser	Glu	Gln	Lys						2420	2425		

<210> 35

<211> 7707

<212> DNA

## &lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 35

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<210> 36

<211> 2696

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 36

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20      25      30
Gly Asn Gly Gln Ser Asn Phe Ser Glu Pro Leu Asn Gly Cys Thr Met
35      40      45
Gln Leu Ser Thr Val Ser Gly Thr Ser Gln Asn Ala Tyr Gly Gln Asp
50      55      60
Ser Pro Ser Cys Tyr Ile Pro Leu Arg Arg Leu Gln Asp Leu Ala Ser
65      70      75      80
Met Ile Asn Val Glu Tyr Leu Asn Gly Ser Ala Asp Gly Ser Glu Ser
85      90      95
Phe Gln Asp Pro Glu Lys Ser Asp Ser Arg Ala Gln Thr Pro Ile Val
100     105     110
Cys Thr Ser Leu Ser Pro Gly Gly Pro Thr Ala Leu Ala Met Lys Gln
115     120     125
Glu Pro Ser Cys Asn Asn Ser Pro Glu Leu Gln Val Lys Val Thr Lys
130     135     140
Thr Ile Lys Asn Gly Phe Leu His Phe Glu Asn Phe Thr Cys Val Asp
145     150     155     160
Asp Ala Asp Val Asp Ser Glu Met Asp Pro Glu Gln Pro Val Thr Glu
165     170     175
Asp Glu Ser Ile Glu Glu Ile Phe Glu Glu Thr Gln Thr Asn Ala Thr
180     185     190
Cys Asn Tyr Glu Thr Lys Ser Glu Asn Gly Val Lys Val Ala Met Gly
195     200     205
Ser Glu Gln Asp Ser Thr Pro Glu Ser Arg His Gly Ala Val Lys Ser
210     215     220
Pro Phe Leu Pro Leu Ala Pro Gln Thr Glu Thr Gln Lys Asn Lys Gln
225     230     235     240
Arg Asn Glu Val Asp Gly Ser Asn Glu Lys Ala Ala Leu Leu Pro Ala
245     250     255

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	290					295					300					
Gln	Glu	Leu	Pro	Phe	Cys	Gln	Pro	Lys	Lys	Lys	Ser	Thr	Pro	Leu	Lys	
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Trp	Pro	Cys	Arg	Ile	Cys	Ser	Asp	Pro	Leu	Ile	Asn	Thr	His	Ser	Lys	
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Arg	Gly	Lys	Gln	Lys	Glu	Lys	Gly	Tyr	Arg	His	Lys	Val	Pro	Gln	Lys	
			405						410					415		
Ile	Leu	Ser	Lys	Trp	Glu	Ala	Ser	Val	Gly	Leu	Ala	Glu	Gln	Tyr	Asp	
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Val	Pro	Lys	Gly	Ser	Lys	Asn	Arg	Lys	Cys	Ile	Pro	Gly	Ser	Ile	Lys	
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Ser	Arg	Ala	Arg	Lys	Ser	Ser	Asp	Asn	Pro	Lys	Arg	Thr	Ser	Val	Lys	
			500					505					510			
Lys	Gly	His	Ile	Gln	Phe	Glu	Ala	His	Lys	Asp	Glu	Arg	Arg	Gly	Lys	
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Ile	Pro	Glu	Asn	Leu	Gly	Leu	Asn	Phe	Ile	Ser	Gly	Asp	Ile	Ser	Asp	
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Thr	Gln	Ala	Ser	Asn	Glu	Leu	Ser	Arg	Ile	Ala	Asn	Ser	Leu	Thr	Gly	
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Ser	Asn	Thr	Ala	Pro	Gly	Ser	Phe	Leu	Phe	Ser	Ser	Cys	Gly	Lys	Asn	
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Pro	Gln	Arg	Ser	Leu	Val	Cys	Gly	Ser	Lys	Val	Lys	Leu	Cys	Tyr	Ile	
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Phe	Ala	Ala	Thr	Asn	Thr	Arg	Val	Lys	Ala	Lys	Gln	Lys	Pro	Leu	Ile	
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Ser	Asn	Ser	His	Thr	Asp	His	Leu	Met	Gly	Cys	Thr	Lys	Ser	Ala	Glu	
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Pro	Gly	Thr	Glu	Thr	Ser	Gln	Val	Asn	Leu	Ser	Asp	Leu	Lys	Ala	Ser	
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Lys	Glu	Leu	Ser	Tyr	Arg	Ser	Leu	Gly	Glu	Asp	Val	Ser	Asp	Ser	Gly		
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Thr	Ser	Lys	Pro	Ser	Lys	Pro	Leu	Leu	Phe	Ser	Ser	Ala	Ser	Ser	Gln		
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Asn	His	Ile	Pro	Ile	Glu	Pro	Asp	Tyr	Lys	Phe	Ser	Thr	Leu	Leu	Met		
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Ala	Ser	Leu	Pro	Gly	Leu	Leu	Ser	Asp	Lys	Arg	Asp	Leu	Pro	Ala	Ser		
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Glu	Arg	Gly	Gly	Ser	Leu	Arg	Gly	Gly	Ala	Glu	Asp	Pro	Ser	Lys	Glu		
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	1090					1095					1100						
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Lys	Ile	Ser	Glu	Lys	Gly	Leu	Ser	Phe	Glu	Asn	Gly	Lys	Gly	Pro	Glu		
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Leu	Asp	Ser	Val	Met	Asn	Ser	Glu	Asn	Asp	Glu	Leu	Asn	Gly	Val	Asn		
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Gln	Val	Val	Pro	Lys	Lys	Arg	Trp	Gln	Arg	Leu	Asn	Gln	Arg	Arg	Thr		
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Lys	Pro	Arg	Lys	Arg	Met	Asn	Arg	Phe	Lys	Glu	Lys	Glu	Asn	Ser	Glu		
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Cys	Ala	Phe	Arg	Val	Leu	Pro	Ser	Asp	Pro	Val	Gln	Glu	Gly	Arg			
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Asp	Glu	Phe	Pro	Glu	His	Arg	Thr	Pro	Ser	Ala	Ser	Ile	Leu	Glu	Glu		
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Pro	Leu	Thr	Glu	Gln	Asn	His	Ala	Asp	Cys	Leu	Asp	Ser	Ala	Gly	Pro	
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Lys	Glu	Pro	Gly	Ile	Pro	Ser	Leu	Thr	Pro	Gln	Ala	Glu	Leu	Pro	Glu	
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Pro	Ala	Val	Arg	Ser	Glu	Lys	Lys	Arg	Leu	Arg	Lys	Pro	Ser	Lys	Trp	
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Lys	Gln	Lys	Lys	Val	Gln	Glu	Gln	Val	His	Lys	Val	Ser	Ser	Arg	Cys	
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Glu	Glu	Glu	Ser	Leu	Leu	Ala	Arg	Gly	Arg	Ser	Ser	Ala	Gln	Asn	Lys	
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Leu	Glu	Arg	Glu	Ala	Pro	Phe	Leu	Glu	Gly	Pro	Leu	Ala	Gln	Ser	Glu	
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Val	Ala	Pro	Glu	Val	Ser	Pro	Arg	Pro	Ala	Leu	Glu	Ser	Glu	Glu	Leu	
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Leu	Val	Lys	Thr	Pro	Gly	Asn	Tyr	Glu	Ser	Lys	Arg	Gln	Arg	Lys	Pro	
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Thr	Lys	Lys	Leu	Leu	Glu	Ser	Asn	Asp	Leu	Asp	Pro	Gly	Phe	Met	Pro	
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Lys	Lys	Gly	Asp	Leu	Gly	Leu	Ser	Lys	Lys	Cys	Tyr	Glu	Ala	Gly	His	
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Leu	Glu	Asn	Gly	Ile	Thr	Glu	Ser	Cys	Ala	Thr	Ser	Tyr	Ser	Lys	Asp	
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Arg	Gln	Arg	His	Ala	Ala	Ala	Lys	Met	Gln	Cys	Lys	Lys	Val	Lys	Asn	
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His	Asp	Pro	Gly	Met	Pro	Ala	Ser	Lys	Lys	Met	Gln	Gly	Glu	Arg	Gly	
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Gly	Glu	Leu	Leu	Leu	Cys	Glu	Ala	Gln	Cys	Cys	Gly	Ala	Phe	His	Leu	
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Glu	Asp	Val	Lys	Arg	Cys	Leu	Leu	Pro	Leu	Cys	Gly	Lys	Phe	Tyr	His	
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Phe	Arg	Cys	Ser	Leu	His	Ile	Cys	Ile	Thr	Cys	His	Ala	Ala	Asn	Pro	
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Ala	Asn	Val	Ser	Ala	Ser	Lys	Gly	Arg	Leu	Met	Arg	Cys	Val	Arg	Cys	
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Pro	Val	Ala	Tyr	His	Ala	Asn	Asp	Phe	Cys	Leu	Ala	Ala	Gly	Ser	Lys	
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Ile	Leu	Ala	Ser	Asn	Ser	Ile	Ile	Cys	Pro	Asn	His	Phe	Thr	Pro	Arg	
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Arg Gly Cys	Arg Asn His	Glu His Val	Asn Val Ser	Trp Cys Phe	Val
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Cys Ser Glu	Gly Gly Ser	Leu Leu Cys	Cys Asp Ser	Cys Pro Ala	Ala
	1715		1720		1725
Phe His Arg	Glu Cys Leu	Asn Ile Asp	Ile Pro Glu	Gly Asn Trp	Tyr
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Cys Asn Asp	Cys Lys Ala	Gly Lys Lys	Pro His Tyr	Arg Glu Ile	Val
	1745		1750		1755
Trp Val Lys	Val Gly Arg	Tyr Arg Trp	Trp Pro Ala	Glu Ile Cys	His
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Pro Arg Ala	Val Pro Ser	Asn Ile Asp	Lys Met Arg	His Asp Val	Gly
	1780		1785		1790
Glu Phe Pro	Val Leu Phe	Phe Gly Ser	Asn Asp Tyr	Leu Trp Thr	His
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Gln Ala Arg	Val Phe Pro	Tyr Met Glu	Gly Asp Val	Ser Ser Lys	Asp
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Lys Met Gly	Lys Gly Val	Asp Gly Thr	Tyr Lys Lys	Ala Leu Gln	Glu
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Ala Ala Ala	Arg Phe Glu	Glu Leu Lys	Ala Gln Lys	Glu Leu Arg	Gln
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Leu Gln Glu	Asp Arg Lys	Asn Asp Lys	Lys Pro Pro	Pro Tyr Lys	His
	1860		1865		1870
Ile Lys Val	Asn Arg Pro	Ile Gly Arg	Val Gln Ile	Phe Thr Ala	Asp
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Leu Ser Glu	Ile Pro Arg	Cys Asn Cys	Lys Ala Thr	Asp Glu Asn	Pro
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Cys Gly Ile	Asp Ser Glu	Cys Ile Asn	Arg Met Leu	Leu Tyr Glu	Cys
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His Pro Thr	Val Cys Pro	Ala Gly Gly	Arg Cys Gln	Asn Gln Cys	Phe
	1925		1930		1935
Ser Lys Arg	Gln Tyr Pro	Glu Val Glu	Ile Phe Arg	Thr Leu Gln	Arg
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Gly Trp Gly	Leu Arg Thr	Lys Thr Asp	Ile Lys Lys	Gly Glu Phe	Val
	1955		1960		1965
Asn Glu Tyr	Val Gly Glu	Leu Ile Asp	Glu Glu Glu	Cys Arg Ala	Arg
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Ile Arg Tyr	Ala Gln Glu	His Asp Ile	Thr Asn Phe	Tyr Met Leu	Thr
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Leu Asp Lys	Asp Arg Ile	Ile Asp Ala	Gly Pro Lys	Gly Asn Tyr	Ala
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Arg Phe Met	Asn His Cys	Cys Gln Pro	Asn Cys Glu	Thr Gln Lys	Trp
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Ser Val Asn	Gly Asp Thr	Arg Val Gly	Leu Phe Ala	Leu Ser Asp	Ile
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Lys Ala Gly	Thr Glu Leu	Thr Phe Asn	Tyr Asn Leu	Glu Cys Leu	Gly
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Asn Gly Lys	Thr Val Cys	Lys Cys Gly	Ala Pro Asn	Cys Ser Gly	Phe
	2065		2070		2075
Leu Gly Val	Arg Pro Lys	Asn Gln Pro	Ile Ala Thr	Glu Glu Lys	Ser
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Lys Lys Phe	Lys Lys Lys	Gln Gln Gly	Lys Arg Arg	Thr Gln Gly	Glu
	2100		2105		2110
Ile Thr Lys	Glu Arg Glu	Asp Glu Cys	Phe Ser Cys	Gly Asp Ala	Gly
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Gln Leu Val	Ser Cys Lys	Lys Pro Gly	Cys Pro Lys	Val Tyr His	Ala
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Asp Cys Leu	Asn Leu Thr	Lys Arg Pro	Ala Gly Lys	Trp Glu Cys	Pro
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Trp His Gln	Cys Asp Ile	Cys Gly Lys	Glu Ala Ala	Ser Phe Cys	Glu
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Ile	Ser	Lys	Leu	Asp	Gly	Arg	Leu	Ser	Cys	Thr	Glu	His	Asp	Pro	Cys	2195	2200	2205
Gly	Pro	Asn	Pro	Leu	Glu	Pro	Gly	Glu	Ile	Arg	Glu	Tyr	Val	Pro	Pro	2210	2215	2220
Pro	Val	Pro	Leu	Pro	Pro	Gly	Pro	Ser	Thr	His	Leu	Ala	Glu	Gln	Ser	2225	2230	2235
Thr	Gly	Met	Ala	Ala	Gln	Ala	Pro	Lys	Met	Ser	Asp	Lys	Pro	Pro	Ala	2245	2250	2255
Asp	Thr	Asn	Gln	Met	Leu	Ser	Leu	Ser	Lys	Lys	Ala	Leu	Ala	Gly	Thr	2260	2265	2270
Cys	Gln	Arg	Pro	Leu	Leu	Pro	Glu	Arg	Pro	Leu	Glu	Arg	Thr	Asp	Ser	2275	2280	2285
Arg	Pro	Gln	Pro	Leu	Asp	Lys	Val	Arg	Asp	Leu	Ala	Gly	Ser	Gly	Thr	2290	2295	2300
Lys	Ser	Gln	Ser	Leu	Val	Ser	Ser	Gln	Arg	Pro	Leu	Asp	Arg	Pro	Pro	2305	2310	2315
Ala	Val	Ala	Gly	Pro	Arg	Pro	Gln	Leu	Ser	Asp	Lys	Pro	Ser	Pro	Val	2325	2330	2335
Thr	Ser	Pro	Ser	Ser	Ser	Pro	Ser	Val	Arg	Ser	Gln	Pro	Leu	Glu	Arg	2340	2345	2350
Pro	Leu	Gly	Thr	Ala	Asp	Pro	Arg	Leu	Asp	Lys	Ser	Ile	Gly	Ala	Ala	2355	2360	2365
Ser	Pro	Arg	Pro	Gln	Ser	Leu	Glu	Lys	Thr	Ser	Val	Pro	Thr	Gly	Leu	2370	2375	2380
Arg	Leu	Pro	Pro	Pro	Asp	Arg	Leu	Leu	Ile	Thr	Ser	Ser	Pro	Lys	Pro	2385	2390	2395
Gln	Thr	Ser	Asp	Arg	Pro	Thr	Asp	Lys	Pro	His	Ala	Ser	Leu	Ser	Gln	2405	2410	2415
Arg	Leu	Pro	Pro	Pro	Glu	Lys	Val	Leu	Ser	Ala	Val	Val	Gln	Thr	Leu	2420	2425	2430
Val	Ala	Lys	Glu	Lys	Ala	Leu	Arg	Pro	Val	Asp	Gln	Asn	Thr	Gln	Ser	2435	2440	2445
Lys	Asn	Arg	Ala	Ala	Leu	Val	Met	Asp	Leu	Ile	Asp	Leu	Thr	Pro	Arg	2450	2455	2460
Gln	Lys	Glu	Arg	Ala	Ala	Ser	Pro	His	Gln	Val	Thr	Pro	Gln	Ala	Asp	2465	2470	2475
Glu	Lys	Met	Pro	Val	Leu	Glu	Ser	Ser	Ser	Trp	Pro	Ala	Ser	Lys	Gly	2485	2490	2495
Leu	Gly	His	Met	Pro	Arg	Ala	Val	Glu	Lys	Gly	Cys	Val	Ser	Asp	Pro	2500	2505	2510
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Lys	Ala	Phe	Leu	Tyr	Glu	Pro	Thr	Thr	Gln	Ala	Ser	Gly	Arg	Ala	Ser	2545	2550	2555
Ala	Gly	Ala	Glu	Gln	Thr	Pro	Gly	Pro	Leu	Ser	Gln	Ser	Pro	Gly	Leu	2565	2570	2575
Val	Lys	Gln	Ala	Lys	Gln	Met	Val	Gly	Gly	Gln	Gln	Leu	Pro	Ala	Leu	2580	2585	2590
Ala	Ala	Lys	Ser	Gly	Gln	Ser	Phe	Arg	Ser	Leu	Gly	Lys	Ala	Pro	Ala	2595	2600	2605
Ser	Leu	Pro	Thr	Glu	Glu	Lys	Lys	Leu	Val	Thr	Thr	Glu	Gln	Ser	Pro	2610	2615	2620
Trp	Ala	Leu	Gly	Lys	Ala	Ser	Ser	Arg	Ala	Gly	Leu	Trp	Pro	Ile	Val	2625	2630	2635
Ala	Gly	Gln	Thr	Leu	Ala	Gln	Ser	Cys	Trp	Ser	Ala	Gly	Ser	Thr	Gln	2645	2650	2655

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<211> 1784

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
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<400> 38

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Arg Leu Leu Glu Glu Asp Thr Pro Arg Tyr Met Arg Ala Ser Asp Pro
      35             40             45
Ala Ser Pro His Ile Gly Arg Ser Asn Glu Glu Glu Glu Thr Ser Asp
      50             55             60
Ser Ser Leu Glu Lys Gln Thr Arg Ser Lys Tyr Cys Thr Glu Thr Ser
65             70             75             80

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 Val Lys Ala Tyr Asp Val Thr Arg Met Val Ser Met Pro Gln Thr Thr  
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 Asp Val Trp His Ile Leu Glu Phe Asp Tyr Ser Arg Leu Pro Lys Gln  
 1330 1335 1340  
 Ser Ile Gly Gln Phe His Glu Gly Asp Ala Tyr Val Val Lys Trp Lys  
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 Phe Met Val Ser Thr Ala Val Gly Ser Arg Gln Lys Gly Glu His Ser  
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 Val Arg Ala Ala Gly Lys Glu Lys Cys Val Tyr Phe Phe Trp Gln Gly  
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 Glu Pro Pro Cys Phe Leu Gln Cys Phe Gln Gly Gly Met Val Val His  
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 Ser Gly Arg Arg Glu Glu Glu Glu Asn Val Gln Ser Glu Trp Arg  
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 Leu Tyr Cys Val Arg Gly Glu Val Pro Val Glu Gly Asn Leu Leu Glu  
 1460 1465 1470  
 Val Ala Cys His Cys Ser Ser Leu Arg Ser Arg Thr Ser Met Val Val  
 1475 1480 1485  
 Leu Asn Val Asn Lys Ala Leu Ile Tyr Leu Trp His Gly Cys Lys Ala  
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 Gln Ala His Thr Lys Glu Val Gly Arg Thr Ala Ala Asn Lys Ile Lys  
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Glu Gln Cys Pro Leu Glu Ala Gly Leu His Ser Ser Ser Lys Val Thr  
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Ile His Glu Cys Asp Glu Gly Ser Glu Pro Leu Gly Phe Trp Asp Ala  
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Leu Gly Arg Arg Asp Arg Lys Ala Tyr Asp Cys Met Leu Gln Asp Pro  
1555 1560 1565  
Gly Ser Phe Asn Phe Ala Pro Arg Leu Phe Ile Leu Ser Ser Ser Ser  
1570 1575 1580  
Gly Asp Phe Ala Ala Thr Glu Phe Val Tyr Pro Ala Arg Ala Pro Ser  
1585 1590 1595 1600  
Val Val Ser Ser Met Pro Phe Leu Gln Glu Asp Leu Tyr Ser Ala Pro  
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Gln Pro Ala Leu Phe Leu Val Asp Asn His His Glu Val Tyr Leu Trp  
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Arg Trp Ala Ser Asp Arg Lys Ser Ala Met Glu Thr Val Leu Gln Tyr  
1650 1655 1660  
Cys Lys Gly Lys Asn Leu Lys Lys Pro Ala Pro Lys Ser Tyr Leu Ile  
1665 1670 1675 1680  
His Ala Gly Leu Glu Pro Leu Thr Phe Thr Asn Met Phe Pro Ser Trp  
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Glu His Arg Glu Asp Ile Ala Glu Ile Thr Glu Met Asp Thr Glu Val  
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Thr Ile Tyr Pro Leu Ala Asp Leu Leu Ala Arg Pro Leu Pro Glu Gly  
1730 1735 1740  
Val Asp Pro Leu Lys Leu Glu Ile Tyr Leu Thr Asp Glu Asp Phe Glu  
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1780

<210> 39  
<211> 6719  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence; note =  
synthetic construct

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<210> 40

<211> 731

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 40

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			20					25				30			
Asn	Leu	Tyr	Gly	Asp	Phe	Phe	Thr	Gly	Asp	Ala	Tyr	Val	Ile	Leu	Lys
		35				40					45				
Thr	Val	Gln	Leu	Arg	Asn	Gly	Asn	Leu	Gln	Tyr	Asp	Leu	His	Tyr	Trp
	50				55					60					
Leu	Gly	Asn	Glu	Cys	Ser	Gln	Asp	Glu	Ser	Gly	Ala	Ala	Ala	Ile	Phe
	65				70					75				80	
Thr	Val	Gln	Leu	Asp	Tyr	Leu	Asn	Gly	Arg	Ala	Val	Gln	His	Arg	
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Gln	His	Val	Gln	Val	Glu	Glu	Gly	Ser	Glu	Pro	Asp	Gly	Phe	Trp	Glu
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Ala	Leu	Gly	Gly	Lys	Thr	Ser	Tyr	Arg	Thr	Ser	Pro	Arg	Leu	Lys	Asp
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Lys	Lys	Met	Asp	Ala	His	Pro	Pro	Arg	Leu	Phe	Ala	Cys	Ser	Asn	Arg
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Ile	Gly	Arg	Phe	Val	Ile	Glu	Glu	Val	Pro	Gly	Glu	Leu	Met	Gln	Glu
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Asp	Leu	Ala	Thr	Asp	Asp	Val	Met	Leu	Leu	Asp	Thr	Trp	Asp	Gln	Val
				645				650						655	
Phe	Val	Trp	Val	Gly	Lys	Asp	Ser	Gln	Glu	Glu	Glu	Lys	Thr	Glu	Ala
			660				665						670		
Leu	Thr	Ser	Ala	Lys	Arg	Tyr	Ile	Glu	Thr	Asp	Pro	Ala	Asn	Arg	Asp
		675				680						685			
Arg	Arg	Thr	Pro	Ile	Thr	Val	Val	Arg	Gln	Gly	Phe	Glu	Pro	Pro	Ser
		690				695					700				
Phe	Val	Gly	Trp	Phe	Leu	Gly	Trp	Asp	Asn	Asn	Tyr	Trp	Ser	Val	Asp
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Pro	Leu	Asp	Arg	Ala	Leu	Ala	Glu	Leu	Ala	Ala					
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<210> 41

<211> 2447

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 41

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&lt;210&gt; 42

&lt;211&gt; 928

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 42

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Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala Ala Ala
1          5          10          15
Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Pro Glu Glu Asp
20          25          30
Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg Leu Glu
35          40          45
Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln Lys Leu
50          55          60
Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys
65          70          75          80
Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys
85          90          95
Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu Asp Glu
100         105         110
Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile Ser Val
115         120         125
His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val
130         135         140
Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala
145         150         155         160
Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln
165         170         175
Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys
180         185         190
Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met
195         200         205
Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu Asp
210         215         220
Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr Lys
225         230         235         240
Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly
245         250         255
Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg
260         265         270
Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val
275         280         285
Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly
290         295         300

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Leu	Val	Thr	Ser	Asn	Gly	Leu	Pro	Glu	Val	Glu	Asn	Leu	Ser	Lys	Arg	305	310	315	320
Tyr	Glu	Glu	Ile	Tyr	Leu	Lys	Asn	Lys	Asp	Leu	Asp	Ala	Arg	Leu	Phe	325	330	335	
Leu	Asp	His	Asp	Lys	Thr	Leu	Gln	Thr	Asp	Ser	Ile	Asp	Ser	Phe	Glu	340	345	350	
Thr	Gln	Arg	Thr	Pro	Arg	Lys	Ser	Asn	Leu	Asp	Glu	Glu	Val	Asn	Val	355	360	365	
Ile	Pro	Pro	His	Thr	Pro	Val	Arg	Thr	Val	Met	Asn	Thr	Ile	Gln	Gln	370	375	380	
Leu	Met	Met	Ile	Leu	Asn	Ser	Ala	Ser	Asp	Gln	Pro	Ser	Glu	Asn	Leu	385	390	395	400
Ile	Ser	Tyr	Phe	Asn	Asn	Cys	Thr	Val	Asn	Pro	Lys	Glu	Ser	Ile	Leu	405	410	415	
Lys	Arg	Val	Lys	Asp	Ile	Gly	Tyr	Ile	Phe	Lys	Glu	Lys	Phe	Ala	Lys	420	425	430	
Ala	Val	Gly	Gln	Gly	Cys	Val	Glu	Ile	Gly	Ser	Gln	Arg	Tyr	Lys	Leu	435	440	445	
Gly	Val	Arg	Leu	Tyr	Tyr	Arg	Val	Met	Glu	Ser	Met	Leu	Lys	Ser	Glu	450	455	460	
Glu	Glu	Arg	Leu	Ser	Ile	Gln	Asn	Phe	Ser	Lys	Leu	Leu	Asn	Asp	Asn	465	470	475	480
Ile	Phe	His	Met	Ser	Leu	Leu	Ala	Cys	Ala	Leu	Glu	Val	Val	Met	Ala	485	490	495	
Thr	Tyr	Ser	Arg	Ser	Thr	Ser	Gln	Asn	Leu	Asp	Ser	Gly	Thr	Asp	Leu	500	505	510	
Ser	Phe	Pro	Trp	Ile	Leu	Asn	Val	Leu	Asn	Leu	Lys	Ala	Phe	Asp	Phe	515	520	525	
Tyr	Lys	Val	Ile	Glu	Ser	Phe	Ile	Lys	Ala	Glu	Gly	Asn	Leu	Thr	Arg	530	535	540	
Glu	Met	Ile	Lys	His	Leu	Glu	Arg	Cys	Glu	His	Arg	Ile	Met	Glu	Ser	545	550	555	560
Leu	Ala	Trp	Leu	Ser	Asp	Ser	Pro	Leu	Phe	Asp	Leu	Ile	Lys	Gln	Ser	565	570	575	
Lys	Asp	Arg	Glu	Gly	Pro	Thr	Asp	His	Leu	Glu	Ser	Ala	Cys	Pro	Leu	580	585	590	
Asn	Leu	Pro	Leu	Gln	Asn	Asn	His	Thr	Ala	Ala	Asp	Met	Tyr	Leu	Ser	595	600	605	
Pro	Val	Arg	Ser	Pro	Lys	Lys	Lys	Gly	Ser	Thr	Thr	Arg	Val	Asn	Ser	610	615	620	
Thr	Ala	Asn	Ala	Glu	Thr	Gln	Ala	Thr	Ser	Ala	Phe	Gln	Thr	Gln	Lys	625	630	635	640
Pro	Leu	Lys	Ser	Thr	Ser	Leu	Ser	Leu	Phe	Tyr	Lys	Lys	Val	Tyr	Arg	645	650	655	
Leu	Ala	Tyr	Leu	Arg	Leu	Asn	Thr	Leu	Cys	Glu	Arg	Leu	Leu	Ser	Glu	660	665	670	
His	Pro	Glu	Leu	Glu	His	Ile	Ile	Trp	Thr	Leu	Phe	Gln	His	Thr	Leu	675	680	685	
Gln	Asn	Glu	Tyr	Glu	Leu	Met	Arg	Asp	Arg	His	Leu	Asp	Gln	Ile	Met	690	695	700	
Met	Cys	Ser	Met	Tyr	Gly	Ile	Cys	Lys	Val	Lys	Asn	Ile	Asp	Leu	Lys	705	710	715	720
Phe	Lys	Ile	Ile	Val	Thr	Ala	Tyr	Lys	Asp	Leu	Pro	His	Ala	Val	Gln	725	730	735	
Glu	Thr	Phe	Lys	Arg	Val	Leu	Ile	Lys	Glu	Glu	Glu	Tyr	Asp	Ser	Ile	740	745	750	
Ile	Val	Phe	Tyr	Asn	Ser	Val	Phe	Met	Gln	Arg	Leu	Lys	Thr	Asn	Ile	755	760	765	
Leu	Gln	Tyr	Ala	Ser	Thr	Arg	Pro	Pro	Thr	Leu	Ser	Pro	Ile	Pro	His	770	775	780	

Ile	Pro	Arg	Ser	Pro	Tyr	Lys	Phe	Pro	Ser	Ser	Pro	Leu	Arg	Ile	Pro
785					790					795					800
Gly	Gly	Asn	Ile	Tyr	Ile	Ser	Pro	Leu	Lys	Ser	Pro	Tyr	Lys	Ile	Ser
			805						810					815	
Glu	Gly	Leu	Pro	Thr	Pro	Thr	Lys	Met	Thr	Pro	Arg	Ser	Arg	Ile	Leu
			820					825					830		
Val	Ser	Ile	Gly	Glu	Ser	Phe	Gly	Thr	Ser	Glu	Lys	Phe	Gln	Lys	Ile
		835					840					845			
Asn	Gln	Met	Val	Cys	Asn	Ser	Asp	Arg	Val	Leu	Lys	Arg	Ser	Ala	Glu
	850					855					860				
Gly	Ser	Asn	Pro	Pro	Lys	Pro	Leu	Lys	Lys	Leu	Arg	Phe	Asp	Ile	Glu
865					870					875					880
Gly	Ser	Asp	Glu	Ala	Asp	Gly	Ser	Lys	His	Leu	Pro	Gly	Glu	Ser	Lys
			885					890						895	
Phe	Gln	Gln	Lys	Leu	Ala	Glu	Met	Thr	Ser	Thr	Arg	Thr	Arg	Met	Gln
			900					905					910		
Lys	Gln	Lys	Met	Asn	Asp	Ser	Met	Asp	Thr	Ser	Asn	Lys	Glu	Glu	Lys
		915					920						925		

<210> 43

<211> 2994

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 43

ttccggtttt	tctcagggga	cgttgaaatt	atttttgtaa	cgggagtcgg	gagaggacgg	60
ggcgtgcccc	gcgtgcgcgc	gcgtcgtcct	ccccggcgct	cctccacagc	tcgctggctc	120
ccgccgcgga	aaggcgtcat	gccgcccaaa	acccccgaa	aaacggccgc	caccgccgcc	180
gctgccgcgc	cggaaccccc	ggcacgcgcg	ccgccgcccc	ctcctgagga	ggaccagag	240
caggacagcg	gccccggagga	cctgcctctc	gtcaggcttg	agtttgaaga	aacagaagaa	300
cctgatttta	ctgcattatg	tcagaaatta	aagataccag	atcatgtcag	agagagagct	360
tggttaactt	gggagaaagt	ttcatctgtg	gatggagtat	tgggagggtta	tattcaaaag	420
aaaaaggaac	tgtggggaat	ctgtatcttt	attgcagcag	ttgacctaga	tgagatgtcg	480
ttcactttta	ctgagctaca	gaaaaacata	gaaatcagtg	tccataaatt	ctttaactta	540
ctaaaagaaa	ttgataccag	taccaaagtt	gataatgcta	tgtcaagact	gttgaagaag	600
tatgatgtat	tgtttgcact	cttcagcaaa	ttggaaagga	catgtgaact	tatatatttg	660
acacaacca	gcagttcgat	atctactgaa	ataaattctg	cattgggtgct	aaaagtttct	720
tggatcacat	ttttattagc	taaaggggaa	gtattacaaa	tggaagatga	tctggtgatt	780
tcatttcagt	taatgctatg	tgtccttgac	tattttatta	aactctcacc	tcccatggtg	840
ctcaaagaac	catataaaac	agctgttata	cccattaatg	gttcacctcg	aacaccaggg	900
cgagggtcaga	acaggagtgc	acggatagca	aaacaactag	aaaatgatac	aagaattatt	960
gaagttctct	gtaaagaaca	tgaatgtaat	atagatgagg	tgaaaaatgt	ttatttcaaa	1020
aattttatata	cttttatgaa	ttctcttgga	cttgtaacat	ctaattggact	tccagagggt	1080
gaaaatcttt	ctaaacgata	cgaagaaatt	tatcttataa	ataaagatct	agatgcaaga	1140
ttatttttgg	atcatgataa	aactcttcag	actgattcta	tagacagttt	tgaaacacag	1200
agaacaccac	gaaaaagtaa	ccttgatgaa	gagggtgaatg	taattcctcc	acacactcca	1260
gttaggactg	ttatgaacac	tatccaacaa	ttaatgatga	ttttaaatcc	agcaagtgat	1320
caaccttcag	aaaatctgat	ttctattttt	aacaactgca	cagtgaatcc	aaaagaaagt	1380
atactgaaaa	gagtgaagga	tataggatac	atcttttaaag	agaaatttgc	taaagctgtg	1440
ggacagggtt	gtgtcgaaat	tggatcacag	cgatacaaac	ttggagttcg	cttgtattac	1500
cgagtaatgg	aatccatgct	taaatcagaa	gaagaacgat	tatccattca	aaatttttagc	1560
aaacttctga	atgacaacat	ttttcatatg	tctttatttg	cgtgcgctct	tgagggttga	1620
atggccacat	atagcagaag	tacatctcag	aatcttgatt	ctggaacaga	tttgtctttc	1680
ccatggattc	tgaatgtgct	taattttaaa	gcctttgatt	tttacaaggt	gatcgaaagt	1740
tttatcaaa	cagaaggcaa	cttgacaaga	gaaatgataa	aacattttaga	acgatgtgaa	1800
catcgaatca	tggaaatccct	tgcattggctc	tcagattcac	ctttatttga	tcttattaaa	1860
caatcaaagg	accgagaagg	accaactgat	caccttgaat	ctgcttgtcc	tcttaattctt	1920

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cctctccaga ataatcacac tgcagcagat atgtatcttt ctctgtgaag atctccaaag 1980
aaaaaagggt caactacgcg tgtaaattct actgcaaagt cagagacaca agcaacctca 2040
gccttccaga cccagaagcc attgaaatct acctctcttt cactgtttta taaaaaagtg 2100
tatcggttag cctatctccg gctaaatata ctttgtgaac gccttctgtc tgagcaccca 2160
gaattagaac atatcatctg gacccttttc cagcacaccc tgcagaatga gtatgaactc 2220
atgagagaca ggcatttgga ccaaattatg atgtgttcca tgtatggcat atgcaaagtg 2280
aagaatatag accttaaatt caaaatcatt gtaacagcat acaaggatct tcctcatgct 2340
gttcaggaga cattcaaacg tgttttgatc aaagaagagg agtatgattc tattatagta 2400
ttctataact cgggtcttcat gcagagactg aaaacaaata ttttgagta tgcttcacc 2460
aggcccccta ccttgtcacc aatacctcac attcctcgaa gcccttacia gtttcctagt 2520
tcacccttac ggattcctgg agggaacatc tatatttcac ccctgaagag tccatataaa 2580
atctcagaag gtctgccaac accaacaaaa atgactccaa gatcaagaat cttagtatca 2640
attggtgaat cattcgggac ttctgagaag ttccagaaaa taaatcagat ggtatgtaac 2700
agcgaccgtg tgctcaaaag aagtgtgtaa ggaagcaacc ctctaaacc actgaaaaaa 2760
ctacgctttg atattgaagg atcagatgaa gcagatggaa gtaaaccatct cccaggagag 2820
tccaaatttc agcagaaact ggcagaaatg acttctactc gaacacgaat gcaaaagcag 2880
aaaatgaatg atagcatgga tacctcaaac aaggaagaga aatgaggatc tcaggacctt 2940
ggtggacact gtgtacacct ctggattcat tgtctctcac agatgtgact gtat 2994

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&lt;210&gt; 44

&lt;211&gt; 782

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence; note =  
synthetic construct

&lt;400&gt; 44

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Met Ala Pro His Arg Pro Ala Pro Ala Leu Leu Cys Ala Leu Ser Leu
1          5          10          15
Ala Leu Cys Ala Leu Ser Leu Pro Val Arg Ala Ala Thr Ala Ser Arg
20          25          30
Gly Ala Ser Gln Ala Gly Ala Pro Gln Gly Arg Val Pro Glu Ala Arg
35          40          45
Pro Asn Ser Met Val Val Glu His Pro Glu Phe Leu Lys Ala Gly Lys
50          55          60
Glu Pro Gly Leu Gln Ile Trp Arg Val Glu Lys Phe Asp Leu Val Pro
65          70          75          80
Val Pro Thr Asn Leu Tyr Gly Asp Phe Phe Thr Gly Asp Ala Tyr Val
85          90          95
Ile Leu Lys Thr Val Gln Leu Arg Asn Gly Asn Leu Gln Tyr Asp Leu
100         105         110
His Tyr Trp Leu Gly Asn Glu Cys Ser Gln Asp Glu Ser Gly Ala Ala
115         120         125
Ala Ile Phe Thr Val Gln Leu Asp Asp Tyr Leu Asn Gly Arg Ala Val
130         135         140
Gln His Arg Glu Val Gln Gly Phe Glu Ser Ala Thr Phe Leu Gly Tyr
145         150         155         160
Phe Lys Ser Gly Leu Lys Tyr Lys Lys Gly Gly Val Ala Ser Gly Phe
165         170         175
Lys His Val Val Pro Asn Glu Val Val Val Gln Arg Leu Phe Gln Val
180         185         190
Lys Gly Arg Arg Val Val Arg Ala Thr Glu Val Pro Val Ser Trp Glu
195         200         205
Ser Phe Asn Asn Gly Asp Cys Phe Ile Leu Asp Leu Gly Asn Asn Ile
210         215         220
His Gln Trp Cys Gly Ser Asn Ser Asn Arg Tyr Glu Arg Leu Lys Ala
225         230         235         240

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Thr	Gln	Val	Ser	Lys	Gly	Ile	Arg	Asp	Asn	Glu	Arg	Ser	Gly	Arg	Ala	
				245					250					255		
Arg	Val	His	Val	Ser	Glu	Glu	Gly	Thr	Glu	Pro	Glu	Ala	Met	Leu	Gln	
			260					265					270			
Val	Leu	Gly	Pro	Lys	Pro	Ala	Leu	Pro	Ala	Gly	Thr	Glu	Asp	Thr	Ala	
		275					280					285				
Lys	Glu	Asp	Ala	Ala	Asn	Arg	Lys	Leu	Ala	Lys	Leu	Tyr	Lys	Val	Ser	
	290					295					300					
Asn	Gly	Ala	Gly	Thr	Met	Ser	Val	Ser	Leu	Val	Ala	Asp	Glu	Asn	Pro	
305					310					315				320		
Phe	Ala	Gln	Gly	Ala	Leu	Lys	Ser	Glu	Asp	Cys	Phe	Ile	Leu	Asp	His	
			325					330						335		
Gly	Lys	Asp	Gly	Lys	Ile	Phe	Val	Trp	Lys	Gly	Lys	Gln	Ala	Asn	Thr	
			340					345					350			
Glu	Glu	Arg	Lys	Ala	Ala	Leu	Lys	Thr	Ala	Ser	Asp	Phe	Ile	Thr	Lys	
		355				360						365				
Met	Asp	Tyr	Pro	Lys	Gln	Thr	Gln	Val	Ser	Val	Leu	Pro	Glu	Gly	Gly	
	370					375					380					
Glu	Thr	Pro	Leu	Phe	Lys	Gln	Phe	Phe	Lys	Asn	Trp	Arg	Asp	Pro	Asp	
385					390					395				400		
Gln	Thr	Asp	Gly	Leu	Gly	Leu	Ser	Tyr	Leu	Ser	Ser	His	Ile	Ala	Asn	
			405					410						415		
Val	Glu	Arg	Val	Pro	Phe	Asp	Ala	Ala	Thr	Leu	His	Thr	Ser	Thr	Ala	
			420					425					430			
Met	Ala	Ala	Gln	His	Gly	Met	Asp	Asp	Asp	Gly	Thr	Gly	Gln	Lys	Gln	
		435				440						445				
Ile	Trp	Arg	Ile	Glu	Gly	Ser	Asn	Lys	Val	Pro	Val	Asp	Pro	Ala	Thr	
	450					455					460					
Tyr	Gly	Gln	Phe	Tyr	Gly	Gly	Asp	Ser	Tyr	Ile	Ile	Leu	Tyr	Asn	Tyr	
465					470					475				480		
Arg	His	Gly	Gly	Arg	Gln	Gly	Gln	Ile	Ile	Tyr	Asn	Trp	Gln	Gly	Ala	
			485					490						495		
Gln	Ser	Thr	Gln	Asp	Glu	Val	Ala	Ala	Ser	Ala	Ile	Leu	Thr	Ala	Gln	
			500					505					510			
Leu	Asp	Glu	Glu	Leu	Gly	Gly	Thr	Pro	Val	Gln	Ser	Arg	Val	Val	Gln	
	515						520					525				
Gly	Lys	Glu	Pro	Ala	His	Leu	Met	Ser	Leu	Phe	Gly	Gly	Lys	Pro	Met	
	530					535					540					
Ile	Ile	Tyr	Lys	Gly	Gly	Thr	Ser	Arg	Glu	Gly	Gln	Thr	Ala	Pro		
545					550					555				560		
Ala	Ser	Thr	Arg	Leu	Phe	Gln	Val	Arg	Ala	Asn	Ser	Ala	Gly	Ala	Thr	
			565					570					575			
Arg	Ala	Val	Glu	Val	Leu	Pro	Lys	Ala	Gly	Ala	Leu	Asn	Ser	Asn	Asp	
		580						585					590			
Ala	Phe	Val	Leu	Lys	Thr	Pro	Ser	Ala	Ala	Tyr	Leu	Trp	Val	Gly	Thr	
	595					600						605				
Gly	Ala	Ser	Glu	Ala	Glu	Lys	Thr	Gly	Ala	Gln	Glu	Leu	Leu	Arg	Val	
	610					615					620					
Leu	Arg	Ala	Gln	Pro	Val	Gln	Val	Ala	Glu	Gly	Ser	Glu	Pro	Asp	Gly	
625					630					635				640		
Phe	Trp	Glu	Ala	Leu	Gly	Gly	Lys	Ala	Ala	Tyr	Arg	Thr	Ser	Pro	Arg	
			645					650						655		
Leu	Lys	Asp	Lys	Lys	Met	Asp	Ala	His	Pro	Pro	Arg	Leu	Phe	Ala	Cys	
		660						665					670			
Ser	Asn	Lys	Ile	Gly	Arg	Phe	Val	Ile	Glu	Glu	Val	Pro	Gly	Glu	Leu	
	675					680						685				
Met	Gln	Glu	Asp	Leu	Ala	Thr	Asp	Asp	Val	Met	Leu	Leu	Asp	Thr	Trp	
	690					695					700					
Asp	Gln	Val	Phe	Val	Trp	Val	Gly	Lys	Asp	Ser	Gln	Glu	Glu	Glu	Lys	
705					710					715					720	

Thr	Glu	Ala	Leu	Thr	Ser	Ala	Lys	Arg	Tyr	Ile	Glu	Thr	Asp	Pro	Ala
				725					730					735	
Asn	Arg	Asp	Arg	Arg	Thr	Pro	Ile	Thr	Val	Val	Lys	Gln	Gly	Phe	Glu
			740					745					750		
Pro	Pro	Ser	Phe	Val	Gly	Trp	Phe	Leu	Gly	Trp	Asp	Asp	Asp	Tyr	Trp
		755					760					765			
Ser	Val	Asp	Pro	Leu	Asp	Arg	Ala	Met	Ala	Glu	Leu	Ala	Ala		
	770					775					780				

<210> 45

<211> 2663

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 45

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gcgcgctgtc	gctgcccgtc	cgcgcgccca	ctgcgtcgcg	gggggcgtcc	caggcggggg	120
cgccccaggg	gcgggtgccc	gaggcgcggc	ccaacagcat	ggtggtggaa	caccccagat	180
tcttcaaggc	agggaaaggag	cctggcctgc	agatctggcg	tgtggagaag	ttcgatctgg	240
tgcccgtgcc	caccaacctt	tatggagact	tcttcacggg	cgacgcctac	gtcatcctga	300
agacagtgca	gctgaggaac	ggaaatctgc	agtatgacct	ccactactgg	ctgggcaatg	360
agtgcagcca	ggatgagagc	ggggcgcccg	ccatctttac	cgtgcagctg	gatgactacc	420
tgaacggccg	ggccgtgcag	caccgtgagg	tccagggtct	cgatcgggcc	accttcctag	480
gctacttcaa	gtctggcctg	aagtacaaga	aaggaggtgt	ggcatcagga	ttcaagcacg	540
tggtagccaa	cgaggtggtg	gtgcagagac	tcttccagggt	caaagggcgg	cgtgtggtcc	600
gtgccaccga	ggtacctgtg	tcctggggaga	gcttcaacaa	tggcgactgc	ttcatcctgg	660
acctgggcaa	caacatccac	cagtgggtgtg	gttccaacag	caatcggtat	gaaagactga	720
agggcacaca	ggtgtccaag	ggcatccggg	acaacgacg	gagtggccgg	gcccagagtgc	780
acgtgtctga	ggagggcact	gagcccagg	cgatgctcca	ggtgctgggc	cccaagccgg	840
ctctgcctgc	aggtaccgag	gacaccgcca	aggaggatgc	ggccaaccgc	aagctggcca	900
agctctacaa	ggtctccaat	ggtgcaggga	ccatgtccgt	ctccctcgtg	gctgatgaga	960
acctcttcgc	ccagggggcc	ctgaagtcag	aggactgctt	catcctggac	cacggcaaag	1020
atgggaaaat	ctttgtctgg	aaaggcaagc	aggcaaacac	ggaggagagg	aaggctgccc	1080
tcaaaacagc	ctctgacttc	atcaccaaga	tggactaccc	caagcagact	caggtctcgg	1140
tccttctctga	gggcggtgag	acccactgt	tcaagcagtt	cttcaagaac	tggcgggacc	1200
cagaccagac	agatggcctg	ggcttgtcct	acctttccag	ccatatcgcc	aacgtggagc	1260
gggtgcccct	cgacgcgcgc	accctgcaca	cctccactgc	catggccgcc	cagcacggca	1320
tggatgacga	tggcacaggc	cagaaacaga	tctggagaat	cgaagggtcc	aacaaggtgc	1380
ccgtggaccc	tgccacatat	ggacagttct	atggaggcga	cagctacatc	attctgtaca	1440
actaccgcca	tgggtggccgc	caggggcaga	taatctataa	ctggcaggggt	gcccagtcta	1500
cccaggatga	ggtcgctgca	tctgccatcc	tgactgtctca	gctggatgag	gagctgggag	1560
gtacccctgt	ccagagccgt	gtggtccaag	gcaaggagcc	cgccacctc	atgagcctgt	1620
ttggtgggaa	gcccattgat	atctacaagg	gcggcacctc	ccgcgagggc	gggcagacag	1680
cccctgccag	caccgcctc	ttccagggtc	gcgccaacag	cgctggagcc	acccgggctg	1740
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<210> 46

<211> 1441

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
 synthetic construct

<400> 46

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Lys	Arg	Met	Glu	Gln	Glu	Lys	Ser	Thr	Thr	Asp	Asp	Asp	Val	Gln	Lys	85	90	95	
Ser	Asp	Ile	Ser	Ser	Ser	Ser	Gln	Gly	Val	Ile	Glu	Lys	Glu	Ser	Leu	100	105	110	
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Cys	Glu	Gly	Arg	Ile	Val	Phe	Val	Ser	Glu	Asn	Val	Thr	Ser	Tyr	Leu	130	135	140	
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His	Thr	Phe	Asn	Cys	Arg	Met	Leu	Ile	His	Pro	Pro	Asp	Glu	Pro	Gly	195	200	205	
Thr	Glu	Asn	Gln	Glu	Ala	Cys	Gln	Arg	Tyr	Glu	Val	Met	Gln	Cys	Phe	210	215	220	
Thr	Val	Ser	Gln	Pro	Lys	Ser	Ile	Gln	Glu	Asp	Gly	Glu	Asp	Phe	Gln	225	230	235	240
Ser	Cys	Leu	Ile	Cys	Ile	Ala	Arg	Arg	Leu	Pro	Arg	Pro	Pro	Ala	Ile	245	250	255	
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<211> 4547

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =  
synthetic construct

<400> 47

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